Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results.file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher

members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or numbers This Page Blank (uspic,



STIC-Biotech/ChemLib

180086

From:

Bunner, Bridget

Sent:

Tuesday, February 21, 2006 3:47 PM

To:

STIC-Biotech/ChemLib

Subject:

sequence search

Hi! I'd like to request a sequence search for case 10/620,642:

- 1. the amino acid sequence of SEQ ID NO: 46
- 2. the amino acid sequence of SEQ ID NO: 61
- 3. the amino acid sequence of SEQ ID NO: 63

Thanks!

Bridget Bunner

Art Unit 1647 Rem 4C65 (571) 272-0881 mailbox 4C70

[3] 21 200

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#_____ AA#:____

S/L:___ Oligomer:____

Encode/Transl:____

Structure #:____Text:__

Inventor:____ Litigation:___

Vendors and cost where applicable
STN:_____
DIALOG:___
QUESTEL/ORBIT:____
LEXIS/NEXIS:___
SEQUENCE SYSTEM:___
WWW/Internet:____
Other (Specify):____



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1030
                                                                                                                            February 22, 2006, 18:05:41; Search time 122.336 Seconds (without alignments) 747.047 Million cell updates/sec
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1061
1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI 208
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                        2443163
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		عد			SUMMAKIES			
Score	- - i	Query	Query Match Length	80	αı	Description	ion	
1061		100.0	208	~	AAR83977	977	Human st	ate
1001		100.0	208	~	AAR95175	Aar95175	Stem	cell
1061		100.0	208	m	AAY53286	Aay53286	Human	ate
1001		100.0	208	4	AAB98355	Aab98355	Human	ste
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		100.0	208	4	AAB96940	Aab96940	Human	ate
		100.0	208	4	AAB73565	Aab73565	Human	SCF
1061		100.0	208	4	AAU02764	Aau02764	Human	SCF
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1061		100.0	208	7	ADE52474	Ade52474	Human	ate
		100.0	208	æ	ADP99316	Adp99316	Human	ste
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		100.0	208	σ	ADW93091	Adw93091	Human	Ste
1061		100.0	208	σ	ADZ47543	Adz47543	Human	ate
1052		99.2	208	~	AAR11710	Aar11710	Human	Ste
1030		97.1	220	0	ADW93154	Adw93154	Human	Ste
1030		97.1	220	σ	ADZ47643	Adz47643	Human	ste
1030		97.1	248	σ	ADW93153	Adw93153	Human	Ste
1030		97.1	248	σ	ADZ47644	Adz47644	Human	Bte
1030		97.1	273	~	AAR11711	Aar11711	Human	Ste
1030		97.1	273	7	AAR20647	Aar20647	Human	mas
1030		97.1	273	7	AAR83978	Aar83978	Human	ste

New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood cells.

REXTTTX

Disclosure, Fig 15C; 127pp; English

Aaw27607 Human rec Aay53284 Human SCF Aab98356 Human SCF Aab98357 Human SCF Aau02460 Human SCF Aau02460 Human SCF Aab96941 Human SCF Aab96941 Human SCF Aab96952 Human SCF Aab73567 Human SCF Aab73567 Human SCF Aau02766 Human SCF Aau02765 Human SCF Aau02765 Human SCF Aau05266 Human SCF Aau05266 Human SCF Aac2224 Human SCF Aac2224 Human SCF Aac2224 Human SCF Aac2246 Human SCF Aac2246 Human SCF Aac2246 Human SCF Aac22477 Human SCF Ade52477 Human SCF	SE	iesis; SCF; anaemia;	unodeficiency; bone graft;		Martin FH;
273 2 AAW27607 273 4 AAB98356 273 4 AAB98356 273 4 AAB98357 273 4 AAB96942 273 4 AAB96942 273 4 AAB96941 273 4 AAB96941 273 4 AAB96942 273 4 AAB96952 273 4 AAB96952 273 4 AAB96952 273 4 AAB96952 273 5 AAB969566 273 5 AAB969566 273 5 AAB9695642 273 5 AAB52366 273 5 AAB5266 273 5 AAB52566 273 5 AAB52476	ALIGNMENT rotein; 208 AA.	d) entry) or (SCF). ogenitor; haematopo	penia, leucopenia, AIDS; immunodeficiency neoplasia; myelosuppression; bone marrow s. Location/Qualifiers 125 /label= sig_peptide 26183 /label= mat_peptide	00105391. 00422383. 00537198. 00573616. US005548.	Bosselman RA, Me
25 1030 97.1 28 1030 97.1 29 1030 97.1 30 1030 97.1 31 1030 97.1 34 1030 97.1 35 1030 97.1 36 1030 97.1 37 1030 97.1 40 1030 97.1 41 1030 97.1 42 1030 97.1 43 1030 97.1 44 1030 97.1 44 1030 97.1 45 1030 97.1	RESULT 1 AAR83977 ID AAR83977 standard, protein;	; 003 996 em em	tt;	11-OCT-1995. 04-OCT-1990; 95EP-(16-OCT-1990; 90US-(24-AUG-1990; 90US-(28-SEP-1990; 90WO-(28-SEP-1990; 90WO-(28-SEP-1990; 90WO-(28-SEP-1990; 90WO-(28-SEP-1990; 90WS-(28-SEP-1990; 90WS-((AMGE-) AMGEN INC. ZBebo KM, SuggB SV, WPI, 1995-346090/45. N-PSDB; AAT04889.

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WPI; 1996-251760/25.
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     AAR83997 is human stem cell factor (SCF). Non-naturally occuring SCF and C-terminally truncated polypeptides stimualte growth of primitive progenitors such as haematopoletic progenitor calls, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for the treating neoplasia, nerve damage, infertility, intestinal damage or myelopoliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                             1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
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                                                                                                                                                                                                Gaps
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Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0
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/label= Sig_peptide
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/label= Mat_protein
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                                                                                                                                                          Sequence 208 AA;
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28-APR-1995;
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A DNA sequence (AAT29489) codes for human stem cell factor (SCF) ... (AAR95175). The full-length SCF transcript consists of 8 exons. A novel splice variant has been identified that appears to arise from the inclusion of a novel exon (see also AAT29488) between exons 3 and 4 of the gene. The resulting frameshift produces a novel SCF consisting of the first 39 amino acids of mature SCF followed by a 33-amino acid C-terminal region (AAR95174). The novel SCF is useful for ensuring correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                     Stem cell factor comprising C-terminal sequence given in specification useful to ensure correct development of pre-implantation embryos before implantation into subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
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                                                                                                                                                     Disclosure; Fig 2; 25pp; English.
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90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
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Matches 208; Conservative
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N-PSDB; AAT29489
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28-SEP-1990;
01-OCT-1990;
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11-JUN-1990;
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27-MAR-2001.
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                                                                                                                                        Amethod has been developed of making haematopoietic cells suitable for administration to a subject. The method comprises: (a) obtaining the member of the subject of the subject of the subject of the subject of the cells and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a polypeptide product having at least part of the primary structural confirmation and one or more of the biological properties of naturally occurring stem cell factor (SCP). The method is useful for stimulating primitive progenitor cells including early haematopoietic progenitor cells including early haematopoietic disorders. The method is useful for treating haematopoietic disorders. The method is useful for expanding early haematopoietic progenitors in syngeneic, allogeneic or autologous bone marrow transplant. SCP is useful for chancing the efficiency of gene therapy based on transfecting haematopoietic stem cells. SCP is also useful for combating the myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing haematopoietic recovery after acute blood loss and as a boost to the immune system for fighting neoplasia (cancer). The present invention
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                                                                      Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell factor; SCF; stem cell factor receptor; blood cell disorder;
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            Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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                                                                                                                      Claim 21; Fig 15C; 123pp; English.
            Bosselmann
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Best Local Similarity 100.
Matches 208; Conservative
           Suggs SV,
                                  WPI; 2000-259135/23.
N-PSDB; AAA13716.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208 AA;
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            Zsebo
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cell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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100.0%; Pred. No. 2e-103;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                            Martin FH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Fig 15C; 210pp; English.
                                                                                                                                                                                                                                                                                         Zsebo KM, Bosselman RA, Suggs
                                       89US-00422383.
90US-00537198.
90US-00573616.
90US-00582701.
92US-00172329.
93US-001429633.
98US-00224681
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Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          into cell in vitro.
                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
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                                                                                                        01-OCT-1990;
25-NOV-1992;
21-DEC-1993;
24-MAY-1995;
12-JAN-1998;
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31-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
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                                                                                                                                                                                                                                                                                                                     Suggs SV, Martin FH;
                                                                 1. 25
/label= Signal_peptide
26. 208
/label= Mature_SCF
                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 15C; 209pp; English.
                                                                                                                                                                                           89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
                                                                                                                                                                        95US-00482918
                                                                                                                                                                                                                                                                                                                        Bosselman RA,
                                                                                                                                                                                                                                                              (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                            2001-298941/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS04121
                                    Homo sapiens
                                                                                                                           US6207417-B1
                                                                                                                                                                        07-JUN-1995;
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01-OCT-1990;
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                                                                 Peptide
                                                                                          Protein
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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFS). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemoglubinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, ALDS and severe combined immunodeficiency (SCID). The present sequence is an SCF described in the
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                                                                                                                                                                                                                                                                                                                                                              Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
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100.0%; Pred. No. 2e-103;
ive 0; Mismatches 0; Indels
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/label= signal_peptide
26. .208
/label= mature_stem_cell_factor
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Human stem cell factor SEQ ID NO: 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zsebo KM, Bosselman RA, Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 15C; 209pp; English.
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                                                                                                                                                                           AAB96940 standard; protein; 208
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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Matches 208; Conservative
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25-NOV-1992;
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Peptide
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eplenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungue disease, Fulminating septicaemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitilise.
                                                                                                                                                                                                                                                                      121 KOLKKSPEREFEFTPEEFFRIFINESIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                              1 MKKTQTWILTCIYLQLLLENPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                 61 MDVLPSHCWISEMVVQLSDSLTDLLDKRSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                        XDLKKSPKSPEPRLFTPBEPPRIFNRSIDAPKOPVVASBTSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder.
                                                                                                                                                1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early hematopoietic progenitor cells.
                                                                                        Match 100.0%; Score 1061; DB 4; Length 208; Local Similarity 100.0%; Pred. No. 2e-103; es 208; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human SCF (stem cell factor) protein encoded by SCF cDNA.
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/label= Signal_peptide
26. .208
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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N-PSDB; AAS04222.
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                                                                  Sequence 208
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
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                                                                                           Query Match
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoletic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's disease.
           Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder.
                                                                                                                                                                                                                                                                                            Human SCF (stem cell factor) protein #2, encoded by SCF cDNA.
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                                                                                                                                  1. .25
/label= Signal_peptide
26. .208
                                                                                                                   KPFMLPPVAASSLRNDSSSSNSKYIYLI
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/label= Mature_SCF
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                                                                                                                                                                                                              AAB73565 standard; protein; 208
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; AAH23899.
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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24-AUG-1990;
01-OCT-1990;
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21-DEC-1993;
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                                  (ZSEB/)
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                   encoded by SCF CDNA. The present invention relates to novel frem cell factors (AAU02761-AAU0277), AAU02779, AAU02797) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides (AAU02777-AAU02794) and the oligonucleotides (AAU02777-AAU02794) and the oligonucleotides (AAU02777-AAU02794) and the oligonucleotides of producide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, dispeminated fungus disease, Pulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disporders such as piebaldism and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                          180
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blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
hypopigmentation disorder; viral disorder; AIDS.
                                                                                                                                                                                                                                                                                                1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMILLKYVPG
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                                                                                                                                                                                                                                                          Gaps
           sequence represents human SCF (stem cell factor) protein
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                                                                                                                                                                                                                                  DB 4; Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human stem cell factor (SCF) protein encoded by SCF cDNA.
                                                                                                                                                                                                                                Query Match 100.0%; Score 1061; DB 4 Best Local Similarity 100.0%; Pred. No. 2e-103; Matches 208; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                   KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU05255 standard; protein; 208 AA
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/label= Mature_SCF
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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                                                                                                                                                                                                            Sequence 208 AA;
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01-OCT-1990;
10-APR-1991;
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11-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
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100.0%; Pred. No. 2e-103;
ative 0; Mismatches 0
                                                                                                                                                                                                                                                                                           Martin FH;
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                                                                                                                                                                                                                                                                                               Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Fig 15C; 210pp; English.
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92US-00982255.
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Matches 208, Conservative
                                                                                                                                                                                                                                                                                               Zsebo KM, Bosselman RA,
                                                                                                       ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                        2001-407312/43
                                                                                                                                      (BOSS/) BOSSELMAN R
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180

KPFMLPPVAASSLRNDSSSSNSKYIYLI 208 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208

181 181 Ź

ABG95641 standard; protein; 208

ABG95641 ID ABG

KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT

121

ઠ 셤 ઠે g haematopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic; antianaemic; antifungal; antimalarial; dermatological; human.

Stem cell factor; SCF; blood-forming system; blood cell disorder;

Human SCF protein sequence encoded by cDNA.

(first entry)

05-DEC-2002

ABG95641;

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The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently comparative of that of naturally occurring SCF to allow possession of haematopoietic biological activity of naturally occurring SCF sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemotherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal canage in a mammal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for thancing transfection of early active polymer polypeptide adduct, for thancing transfer of a gene into a mammal. They are useful for treating myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, catederer-siwe disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-siwe disease, refractory erythroblastic anaemia, pigulantary splenic pancytopaenia, disseminated fungus disease, malaria, military cuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12 and folic acid deficiency, Damond Blackfan anaemia, hypopigmentation disorders such as piebaldism, ALDS (acquired immune deficiency syndrome) and vitiligo. The present sequence is human SCF protein
acquired immune deficiency syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency; Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel non-naturally-occurring stem cell factor polypeptide, useful treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
                                                                                                                                                                                                                          /note= "Human mature SCF protein"
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                                                                                                                                                          1. .25
/label= Signal-peptide
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                                                                                                                                   Location/Qualifiers
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(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
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SUGG/) SUGGS S V.
MART/) MARTIN F H.
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                                                                                            Homo sapiens
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                                                                                                                                                     Peptide
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The present invention relates to novel stem cell factors (SCFB), polynucleotide sequences encoding the SCFB, and methods of producing polynucleotide sequences encoding the SCFB, and methods of producing mammals, particularly humans. The method of the invention is useful for the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence represents human SCF
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sculturing
to DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of a human stem cell factor (SCF) polypeptide for disorders involving blood cells, such as leukemia, comprises omammalian cells comprising non-human SCF promoter DNA linked tencoding the human SCF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 15C; 120pp; English.
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N-PSDB; ABS73858.
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Best Local Similarity 100.
Matches 208; Conservative
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Martin

Bosselman RA,

Zsebo KM, Suggs SV,

(AMGE-) AMGEN INC.

90WO-US005548. 90US-00589701. 90EP-00310899. 95EP-00105391.

01-OCT-1990; 04-OCT-1990; 04-OCT-1990;

89US-00422383 90US-00537198.

16-OCT-1989; 11-JUN-1990; 28-SEP-1990

04-OCT-1990; 2002EP-00008587

Homo sapiens

EP1241258-A2 18-SEP-2002, ö

Gaps

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    .25
    /note= "Signal peptide"

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                                                                                                                                           Local Similarity 100.
nes 208; Conservative
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                                                                                                             Sequence 208 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoietic activity and the polynucleotides encoding them. The polypeptides are used for treating infertility, intestinal damage, myeloproliferative discreders, leucopenia, thrombocytopenia or anaemia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of
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                                                                                                                                                                                                                                                                                      Human; stem cell factor; SCF; haematopoietic activity; infertility; intestinal damage; myeloproliferative disorder; leucopenia; thrombocytopenia; anaemia; bone marrow transplant; immune deficiency; neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia; miliary tuberculosis; haematopoietic progenitor cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-natural stem cell factor, useful for treating e.g. leucopenia nne deficiency, also related nucleic acid and antibodies.
                     MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                     KDLKKSPKSPEPRLFTPEEFFRIFMRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
          MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                  MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to stem cell factor (SCF) polypeptides with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                   Human stem cell factor (SCF) polypeptide #2.
                                                                                                                                              KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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91US-00684535.
92US-00982255.
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95US-00449653
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BOSSELMAN R A.
SUGGS S V.
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25-NOV-1992;
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12-JAN-1998;
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KW Human, SCF; stem cell factor; gene therapy;
KW haematopoietic progenitor cell; aplastic anaemia;
KW haematopoietic progenitor cell; aplastic anaemia;
KW paroxysmal nocturnal haemoglobinuria; myelofibrosis; myelosclerosis;
KW osteopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma;
KW hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia;
KW pi duglielmo syndrome; congestive splenomegaly; Kala awar; sarcoidosis;
KW primary splenic pancytopaenia; miliary tuberculosis;
KW primary splenic pancytopaenia; miliary tuberculosis;
KW vitamin B12 deficiency; folic acid deficiency; pyridoxine deficiency;
KW biamond Blackfan anaemia; hypopigmentation disorder; piebaldism;
Vitiligo; neurological damage; infertility; intestinal damage;
KW acute blood loss; neoplasm; cancer.
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immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF polypeptides can be used for recombinant expression of the polypeptides and also as probes for mapping of the SCF gene, for identifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents an SCF polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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100.0%; Pred. No. 2e-103;
ive 0; Mismatches 0
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The invention relates to preparing a (vertebrate) human stem cell factor (SCP) polyapetide comprising growing host cells transformed or transfected with DNA encoding a human SCP that stimulates growth of transfected with DNA encoding a human SCP that stimulates growth of transfected with DNA encoding a nutrient conditions, the DNA being operatively linked to an expression control sequence, and isolating the polyapetide produced. Also included is a recombinant host cell transfected with an expression control sequence, operatively linked to a long to retrebrate SCP polyapetide in the host cell. Disclosed as new are rat and human nuclet acids encoding SCP, SCP protein fragments. The DNA numan nuclet acids encoding SCP, SCP protein fragments. The DNA equence of cell plasmid DNA vectors, new and useful viral and human nuclet acids encoding SCP, SCP protein fragments. The DNA equence of and circular plasmid DNA vectors, new and useful viral transformed and transferred prokaryotic and enkaryotic host cells, and new and useful wariety of recombinant techniques or for generating new and useful viral cransfected prokaryotic and enkaryotic host cells, and new and useful methods for cultured growth of such host cells, and new and useful methods for cultured growth of such host cells, and new and useful methods for cultured growth of such host cells, and new and useful methods for cultured growth of such host cells, and new and useful and probes in isolating human genetic therapy in humans and other mammals, and companies and its related products. The DNA sequences are also useful as a protein synthesis, in genetic therapy in humans and other mammals, and and an accompanies are useful for treating heamatopoletic disoders, e.g., aplastic ansamia, paroxysmal nocturnal heamoglobinuria, myelocitesis, myelocitences, of disorders and disease, lymphona, congestive splences and disease, lymphona, congestive splences and disease, of disorders such as piebaldism and vitiligor. The SCF are also useful for treating neurological damage,
                                                                                                                                                                                                                                                                                                                                       Preparing a human stem cell factor (SCF) polypeptide, useful for treating hematopoietic disorders, e.g., aplastic anemia, comprises growing host cells transformed or transfected with DNA encoding a human SCF.
                                                                                                                                                                                                                                   Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 46; 210pp; English.
                                                                                                                                                                                                                                   Suggs SV,
89US-00422383.
90US-00537198.
90US-00589701.
91US-00684535.
92US-00982255.
93US-00172229.
                                                                                                                                                                                                                                Zsebo KM, Bosselman RA,
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                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                N-PSDB; ADP99315.
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                                                                                                    25-NOV-1992;
21-DEC-1993;
24-MAY-1995;
                                                                                10-APR-1991;
                                             24-AUG-1990
                                                               01-OCT-1990
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Claim 9; SEQ ID NO 46; 216pp; English. Suggs SV, Ŗ, ZSEBO K M. BOSSELMAN R A. SUGGS S V. Zsebo KM, Bosselman WPI; 2004-707481/69. MARTIN F H. transplantation. (ZSEB/) (BOSS/) (SUGG/) (MART/) ö 120 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 1 MKKTQTWILITCIYLQLLEPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG Gaps ö Length 208; Indels DB 8; ö 100.0%; Score 1061; DB 8 100.0%; Pred. No. 2e-103; ive 0; Mismatches 0 Query Match Best Local Similarity 100. Matches 208; Conservative 61

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Novel stem cell factor (SCF) such as non-naturally-occurring SCF or naturally occurring SCF, useful for treating leukopenia, thrombocytopenia, anemia, and enhancing engraftment of bone marrow during
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occurring SCF having an amino acid sequence sufficiently duplicative of
that of naturally occurring SCF to allow possession of a haematopoietic
biological activity of naturally occurring stem cell factor, or naturally
occurring SCF. Also included are an isolated DNA sequence for use in
securing expression in a prokaryotic or eukaryotic host cell of non-
naturally occurring SCF, a prokaryotic or eukaryotic host cell
                                                                                                                                                                                                                                                                                       Human; stem cell factor; SCF; haematopoietic;
HT1080 fibrosarcoma cell line; 5637 bladder carcinoma cell line;
HT1080 fibrosarcoma cell line; 5637 bladder carcinoma cell line;
leukopaenia; thrombocytopaenia; anaemia; bone marrow during transplant;
bone marrow aplasia; myelosuppression; immune deficiency; neoplasm;
nerve damage; infertility; intestinal damage;
myeloproliferative disorder; early haematopoietic progenitor cell;
haematopoietic disorders; aplastic anaemia; myelofibrosis;
myelosclerosis; osteopetrosis; metastatic carcinoma; multiple myeloma;
Hodgkin's disease; lymphoma; daucher's disease; Niemann-Pick disease;
Diamond-Blackfan anaemia; DBA; Panconi's anaemia; gene therapy;
                                                                                                                                                                                                                                                            Human stem cell factor, full length protein #1.
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                                                           KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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2000US-00635249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   acute blood loss.
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07-JUN-1995;
07-AUG-2000;
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01-OCT-1990;
10-APR-1991;
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transformed or transfected with the DNA, a polypeptide product of the expression of the DNA in a prokaryotic or eukaryotic host cell, an isolated DNA sequence coding for provaryotic or eukaryotic host cell, an isolated DNA sequence coding for a provaryotic or eukaryotic host cell, an isolated DNA sequence coding for a provaryotic or eukaryotic host cell factor, a biologically functional plasmid or viral DNA vector cell factor, a biologically functional plasmid or viral DNA vector cell factor, a biologically functional plasmid or viral DNA vector cell factor, a biologically functional plasmid or viral DNA vector cell factor, a biologically functional plasmid or viral DNA vector cell factor, a biologically functional plasmid or viral DNA vector cell cardino acid sequence encoded by composite nucleic acid sequence of human SCF CDNA obtained from #1000 fibrosarcoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell line (and having one or more of in vitro biological carcinoma cell vitro harmal y corcurring stem cell factor, and an antibody (Ab) specifically binding SCF. SCF is useful for treating permeters and enhancing engraftment of bome marrow transplantation in a mammal. SCF is useful enhancing bome marrow cecovery in treatment of radiation, chemical, or chemotherapeutic influence carcinoma and myelosuppression which involves treating perfective doses of SCF. SCF is useful for treating early haematopoietic progenitor cells with a gene which transfecting early haematopoietic progenitor cells with a gene to ammmal which involves culturing early haematopoietic progenitor cells with a gene of ammmal with involves culturing early haematopoietic progenitor cells with a gene of ammmal with involves culturing early haematopoietic progenitor cells with a gene of ammmal with involves culturing early hae

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Antianemic; Antiemetic; Cytostatic; Anti-HIV; Cardiovascular-Gen.; CNS-Gen.; Antiparasitic; Antibacterial; Immunosuppressive; Antiinflammatory; Fungicide; Antifertility; AIDS; aplastic anemia; paroxysmal nocturnal hemoglobinuria; osteopetrosis; acute leukemia; multiple myeloma; hodgkins disease; lymphoma; gauchers disease;
                                  ADW93091 standard; protein; 208 AA
                                                                                                                                            Human Stem Cell Factor, SEQ ID 46.
                                                                                                         (first entry)
                                                                                                           21-APR-2005
                                                                       ADW93091;
RESULT 15
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Stimulating proliferation of melanocyte cells in human, involves administering stem cell factor polypeptide or its biologically active fragments stimulating growth of melanocyte cells, and optionally carrier, to human. niemann pick disease; sarcoidosis; plasmodium infection; vitamin deficiency; hypopigmentation; vitiligo; infertility; chronic myelocytic leukemia; cell proliferation; Stem Cell Fa Suggs SV, Martin FH; 1. .25 /label= Signal_peptide /label= Mature_protein Location/Qualifiers 89US-00422383. 90US-00537198. 90US-00573616. 90US-00684535. 92US-0017323. 93US-0017323. 26-JUN-2000; 2000US-00604325 Zsebo KM, Bosselman RA, .208 WPI; 2005-160562/17. (AMGE-) AMGEN INC. N-PSDB; ADW93090 24-AUG-1990; 01-OCT-1990; 10-APR-1991; 25-NOV-1992; 21-DEC-1993; Homo sapiens US6852313-B1 24-MAY-1995; 16-OCT-1989; 08-FEB-2005 11-JUN-1990 Protein Peptide Κeγ

The present invention relates to a method (M1) for stimulating proliferation of melanocyte cells in a human. (M1) involves administering a Stem Cell Factor (SCF) protein, or its biologically active fragments that stimulates growth of melanocyte cells, and optionally a carrier, to the tsimulates growth of menancyte cells, and optionally a carrier, to the human. The SCF is covalently conjugated to a water soluble polymer corp corp of the cytokines. SCF is also able to stimulate the growth of primitive progenitors such as early hematopoidetic progenitor cells that are capable of maturing to erythroid, megakaryocyte, granulocyte, are capable of maturing to erythroid, megakaryocyte, granulocyte, crymphocyte and macrophage cells, and non-hematopoidetic stem cells that eventual stem cells and primordial germ stem cells (M1) is useful in accelerating bone marrow regeneration, and in augmenting T cell accelerating bone marrow regeneration, and in augmenting T cell accelerating bone marrow regeneration, and in augmenting T cell accelerating by a reduction in functional marrow mass due to toxic, radiant or immunological injury. (M1) is useful in treating AIDS, aplastic anemia, parcysmal nocturnal hemoglobinuria, wylofibrosis, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann Prick disease, congestive splenomegaly, Kalazar, sarcoidosis, primary complexic pancytopenia, disease, lymphoma, Gaucher's disease, prindaring and vitiligo. (M1) is useful in treating infertility states, pricketinal damage resulting from irradiation or chemotherapy, and stem cell myelopachism and acute leukemia. (M1) is useful in expanding call hematopoletic progenitors in syngeneic, allogeneic or autologous bone marrow transplantation, and in enhancing the efficacy of gene constitution, and in enhancing the efficacy of gene Claim 2; SEQ ID NO 46; 212pp; English.

Sequence 208 AA;

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        Query Match
        100.0%; Score 1061; DB 9; Length 208;

        Best Local Similarity 100.0%; Pred. No. 2e-103;
        Aatches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

        QY
        1 MKKTQTWILTCITYQLILENPLYKTEGICRNRYTNNYKOVTKLVANLEKDYMITLKKYPG 60

        Db
        1 MKKTQTWILTCITYQLLENPLYKTEGICRNRYTNNYKOVTKLVANLEKDYMITLKKYPG 60

        QY
        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLWNIVDDLVECVKENSS 120

        Db
        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLWNIVDDLVECVKENSS 120

        CQY
        121 KDLKKSFKSPEPRLFTPEBFFRIFNRSIDAFVDFVVASETSDCVVSSTLSPEKDSRVSVT 180

        Db
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        CQY
        121 KDLKKSFKSPEPRLFTPREFFRIFNRSIDAFYDFVVASETSDCVVSSTLSPEKDSRVSVT 180

        CQY
        181 KPFMLPPVAASSLRNDSSSSNSKYTVII 208

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February 22, 2006, 18:13:23; Search time 17.1901 Seconds (without alignments) 1164.223 Million cell updates/sec Run on:

US-10-620-642-46 1061 1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI 208 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mast cell growth f	æ	mast cell growth f	cell	_		cell	cell	mast cell growth f	stem cell factor -	cell	stem cell factor p	cell	cell	mast cell growth f	- ()				ㅁ	citrate (pro-3S)-1	SEC21 protein - ye		ATP-dependent Clp	phorbol ester-bind	orf2 protein - Jun	phosphoenolpyruvat	K18 antigen - Enta	flagellar hook-len
SUMMARIES	OI 8	A3	: I46575	: B61190	S47571	2 \$58313	: I46929		S65801	. A37934	S29052		: JN0637	S70367			: T16086	F82909	2 T27886	T19295	B69616	: G86773		: S61667	: A69136	2 A41101	: B44054	2 H84855		: H97165
	Length DB	:	274					201														512 2							•	465 2
عان	Query	97.1	84.8	83.9	83.6	83.5	81.3	80.8	80.6	67.4	54.3	53.8	53.0	45.2	16.5	16.3	9.5	9.1	8.9	8.9	8.7	8.7	8.7	9.8	8.5	8.4	8.3	8.3	8.3	8.3
	Score	1030	899.5	890	886.5	885.5	862.5	857	855	715	576.5	570.5	562.5	479.5	175.5	172.5	97.5	97	94	94	92.5		92	91	90.5	89	œ	88.5	88	88
	Result No.	1	7	n	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

membrane-associate	DNA-directed RNA p	probable protein k	phosphoenolpyruvat	hypothetical prote	hypothetical prote	protein F28J9.3 (i	BRO1 protein - yea	hypothetical prote	molybdenum ABC tra	threonine synthase	hypothetical prote	hypothetical prote	hypothetical prote	probable protein k	merozoite surface
F97352	T31670	T04005	S26235	T16411	T19850	F86486	S61104	T08607	A64579	G86887	T22794	T19493	T29762	B86461	A45949
8	7	~	~	~	~	~	~	7	н	N	N	~	7	7	~
702	1690	649	996	664	246	436	844	1271	246	496	660	1334	222	614	636
8.3	8.3	8.5	8.2	8.2	8.2	8.5	8.2	8.2	8.1	8.1	8.1	8.1	8.1	8.1	8.1
88	88	87.5	87.5	87	86.5	86.5	86.5	86.5	98	98	98	98	85.5	85.5	85.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Molecule type: mRNA A;Residues: 1-273 «MAX» A;Cross-references: UNIPROT:P21583; UNIPARC:UPI000002D482; GB:M59964; NID:g337933; PIDN B;Anderson, D.M.; Williams, D.E.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, I Cell Growth Differ. 2, 373-378, 1991 A;Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiz A;Reference number: A61190; MUID:92172791; PMID:1724381

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-273 <AND>
A;Residues: 1-273 <AND>
A;Cross-references: UNIPARC:UPI00002D482

C,Genetics: A,Gene: GDB:MGF A,Cross-references: GDB:128026; OMIM:184745

A; Map position: 1242-12422
C; Superfamily: mouse mast cell growth factor
C; Superfamily: mouse mast cell growth factor
C; Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pr.
C; Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pr.
C; Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane pr.
F; 1-25; Domain: signal sequence #status predicted <NGS>
F; 26-18; Product: (or 26-190) mast cell growth factor, soluble form #status predicted <% S15-237/Domain: transmembrane #status predicted <% Covalent) #status predicted

ö Gaps ö 97.1%; Score 1030; DB 2; Length 273; 99.5%; Pred. No. 4.2e-74; Artive 0; Mismatches 1; Indels 1; Indels Matches 202; Conservative Local Similarity

61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISBGLSNYSIIDKLVNIVDDLVECVKENSS 120 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKRNSS 120 1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60 9 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 61 ò 원 ð

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A;Molecule type: mRNA
A;Residues: 1-274 <ZHO-
A;Cross-references: UNIPROT:Q28132; UNIPARC:UPI0000135639; EMBL:D28934; NID:g538520; PIC
C;Superfamily: mouse mast cell growth factor
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C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c; defector, longer isoform - bovine (species: Bos prinigenius taurus (cattle) (c; Species: Bos prinigenius taurus (cattle) (c; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004 (c; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004 (c; Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004 (c; Dates) (c; D
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58313
R;McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
B;McInnes, C.D.; Dogan, M.; Palconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
A;Description: Molecular Library, August 1995
A;Description: Molecular cloning and biological activity of ovine stem cell factor.
A;Reference number: S58313
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85.3%; Pred. No. 9.1e-63;
iive 16; Mismatches 13
Mismatches
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A; Molecule type: mRNA
A; Residues: 1-202 <MCI>
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NyAlternate names: kit ligand, short form; stem cell factor, short form
C; Specias: Homo sapians (man)
C; Date: O3-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C; Accession: B61190
A; Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza
A; Accession: B61190
A; Cossion: B61190
A; 
                                                                                                                                                                                                                                                                                                                                                                          c-kit ligand - pig
c-kit ligand - pig
c'species: Sus acrofa domestica (domestic pig)
c'species: Sus acrofa domestica (domestic pig)
c'scession: 146575
R'zhang, Z.; Anthony, R.V.
Biol. Reprod. 50, 95-102, 1994
A'THIE: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization w
A'Reference number: 146575; MUID:94146218; PMID:7508758
A'Accession: 146575; MUID:94146218; PMID:7508758
A'Accession: 146575
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Best Local Similarity 86.3%; Pred. No. 8.5e-64;
Matches 176; Conservative 17; Mismatches 10; Indels
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100.0%; Pred. No. 4.2e-63;
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Best Local Similarity
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J. Biol. Chem. 266, 8102-8107, 1991
A;Title: Amino acid sequence and post-translational modification of stem cell factor isc. A;Reference number: A39805; MUID:91217037; PMID:1708771
A;Accession: A39805
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'E',27-190 cLUA>
A;Residues: 'E',27-190 cLUA>
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mast cell growth factor - mouse
NyAlternate names: hematopoietic growth factor KL; ligand steel factor; stem cell facto.
C;Species Mus musculus (house mouse)
C;Decies 28-Oct-1996 #sequence revision 27-Feb-1997 #text change 09-Jul-2004
C;Accession: S65801; A43751; A35976; A35972; A35975; A35973; I48768
R;Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A;Title: Multiple pathways for Steel regulation suggested by genomic and sequence analy.
A;Reference number: S65801; MUID:97002551; PMID:8849898
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A/Andlecule type: mRNA
A;Readiues: 1-273 «BED>
A;Cross-references: UNIPROT:P20826; UNIPARC:UPI0000028C9B; EMBL:U44725; NID:gl172215; P!
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Mol. Biol. Cell 3, 349-352, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit-A;Reference number: A43751; MUID:92330001; PMID:1378327
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A; Residues: 1-214, T. (216-273 <HUA>
A; Residues: 1-214, T. (216-273 <HUA>
A; Cross-references: UNIPARC: UP1000014D0C1; GB: S40364; NID: 9251668; PIDN: AAB22554: 2; PID
A; Note: the authors translated the codon TTG for residue 215 as Trp
R; Huang, E.; Nocka, K.; Beier, D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Ledex
Cell 63, 255-233, 1990
A; Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the ligan
A; Reference number: A35976; MUID: 91004221; PMID: 1698557
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A;Cross-references: UNIPARC:UPI000017955D; GB:M38511
R;Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March, Call 63, 235-243, 1990
A;Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in A;Reference number: A35977; MUID:91004223; PMID:1698558
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80.8%; Score 857; DB 2; Length 20
Best Local Similarity 82.6%; Pred. No. 1.3e-60;
Matches 166; Conservative 15; Mismatches 20; Indels
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C;Species: Rattus norregicus (Norway rat)

C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004

C;Accession: B35974; A39805

R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.

Call 63, 203-211, 1990

A;Title: Primary structure and functional expression of rat and human stem cell factor D

A;Reference number: A35974; MUD:91004219; PMID:2208279

A;Reference number: B35974

A;Residues: 1-201 cMAR>

A;Molecule type: mRNA

A;Residues: 1-201 cMAR>

A;Residues: 1-201 cMAR>

A;Cross-references: UNIPROT:P21581; UNIPARC:UPI0000144090; GB:M59966; NID:g206861; PIDN:

R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zsebo,
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CiSpecies: Canis lupus familiaris (dog)
CiSpecies: Canis lupus familiaris (dog)
CiSpecies: Oails lupus familiaris (dog)
CiSpecies: Oails lupus familiaris (dog)
CiAccession: 146229
KiShull, R.M.; Suggs, S.V.; Langley, K.B.; Okino, K.H.; Jacobsen, F.W.; Martin, F.H.
Exp. Hematol. 20, 1118-1124, 1992
A; Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles canine stem cell factor (c-kit ligand) supports the survival of hematopoietic particles preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuals: 1-274 csHu3
A; Cross-references: UNIPROT: O06220; UNIPARC: UPI000013563A; GB:S53329; NID: g262240; PIDN: C; Superfamily: mouse mast cell growth factor
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                                                                     MKKTOTWI ITCIYLOLLLFNPLVKTKGICGKRVTDDVXDVTKLVANLPKDYKIALKYVPG
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Cell 64, 1025-1035, 1991
Affile: Transmembrane form of the kit ligand growth factor is determined by alternative A;Reference number: A37934; MUID:91160046; PMID:1705866
A;Accession: A37934
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-245 <FLAA
A; Cross-recences: UNIPROT: P20826; UNIPARC: UPI000002B352; GB: M64262
A; Cross-recences: UNIPROT: P20826; UNIPARC: UPI000002B352; GB: M64262
Mol. Biol. Cell 3, 349-362, 1992
Mol. Biol. Cell 3, 349-362, 1992
A; Title: Differential expression and processing of two cell associated forms of the kit-A; Reference number: A43751; MUID: 92330001; PMID: 1378327
                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-173, R',175-186,'L',188-245 <HUA>
A;Cross-references: UNIPARC:UPI0000179560; GB:S04534
A;Note: the authors translated the codon TTG for residue 187 as Trp
C;Superfamily: mouse mast cell growth factor
                  ; Chan, D.C.; Leder, P.
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A;Residues 1-273 cAND>
A;Residues 1-273 cAND>
A;Residues 1-273 cAND>
A;Residues 1-273 cAND>
A;Cross-references UNIFRAC.UPI0000028C9B; GB:NF7647, GB:N38436; NID:g199151; PIDN:AAA33 R;Copeland, NG.; GGlber, D.J.; Cho, B.C.; Donovan, P.J.; denkins, N.A.; Cosman, D.; An A;Residued, NG.; GGlber, D.J.; Cho, B.C.; Donovan, P.J.; denkins, N.A.; Cosman, D.; An A;Residue: A5372
A;Recension: A5375
A;Residue: Zef. Acop
A;Residue: A5375
A;Residue: A5377
A;Residue: A5477

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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N;Alternate names: KL-2 protein
C;Species: Mus musculus (house mouse)
C;Date: 26-Uul-1991 #sequence_revision 26-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37934; B43751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWIITCIYLQLLFRPLVKTKEICGNPVTDNVKDITKLVANLPNDYMITLNYVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.6%; Score 855; DB 2; Best Local Similarity 82.3%; Pred. No. 2.8e-60; Matches 167; Conservative 16; Mismatches 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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stem cell factor - human (fragments)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S29052
R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J.; Langley, K.S.
Jangley, K.S.
Arch. Blochem. Blophys. 298, 150-158, 1992
A;Title: Post-translational processing of membrane-associated recombinant human stem cel A;Reference number: S29052; MUID:92398336; PMID:1381905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: $29052
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
A,Residues: UNIPROT:Q7M4N8; UNIPARC:UPI0000179563; UNIPARC:UPI0000179564; UNIPARC
A,PARC:UPI000017956A
C,Superfamily: mouse mast cell growth factor
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                                                                                                                                                                                                                                                     MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                  61 MDVLPSHCWLRDMVIQLSLSLTTLLDKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGICRNRVINNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 41;
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 576.5; DB 2; Length 124;
Pred. No. 1e-38;
0; Mismatches 0; Indels 41.
Query Match 67.4%; Score 715; DB 2; Length 245; Best Local Similarity 79.8%; Pred. No. 2.8e-49; Matches 138; Conservative 16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vuery Match 54.3%;
Best Local Similarity 75.2%;
Matches 124; Conservative 0
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mast cell growth factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: B35971
R;Williams, D.B.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, J A;Title: Identification of a ligand for the c-kit proto-oncogene.
A;Title: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipectes Coulding Accession: Advant,
Cipectes Colone-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
CiAccession: S70367 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
CiAccession: S70367 #sequence_revision of Colone Cipectes Colone Cipectes 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 NSSKO-LKKSPKSPERPREFEREFRIFURSIDARSDAVASETSDCVVSSTL-SPEKDS 175
::||::|::||:||:||::||
61 MDVLPSHCWISEMVVQLSDSLTDLLDKF---SNISEGLSNYSIIDKLVNIVDDLVECVKG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Coturnix coturnix (quail)
Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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C;Superfamily: mouse mast cell growth factor
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.2%; Score 479.5; DB 2; Best Local Similarity 46.9%; Pred. No. 1.2e-30; Matches 100; Conservative 42; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.5%; Score 175.5; DB 2; Best Local Similarity 72.3%; Pred. No. 1.6e-07; Matches 34; Conservative 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 RVSVTKPFMLPPVAASSLRNDSSSSNSKYIYLI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - quail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stem cell factor short form precursor
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A;Molecule type: protein
A;Residues: 1-51 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: B35971
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C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Species: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 09-Jul-2004
C; Sacession: JN0637
R; Zhou, J.H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A; Title: Sequence of a cDNA encoding chicken stem cell factor.
A; Reference number: JN0637; MUID:93273244; PMID:7684722
A; Reference number: JN0637; MUID:93273244; PMID:7684722
A; Residues: 1-287 < ZHO>
A; Residues: 1-287 < ZHO
A; Residues: 1-287 <
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                                                                                                                                   C;Species: Coturnix coturnix (quain)
C;Species: Coturnix coturnix (quain)
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
R;Accession: S0366
R;Petitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A;Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell facta A;Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell facession: S70366
A;Rocession: S70366
A;Rocession: S70366
A;Rocession: UNIPARC:UPI000013563D; EMBL:U43078; NID:gl150875; PIDN:AAC59933.1; IC;Superfamily: mouse mast cell growth factor
C;Superfamily: mouse mast cell factor
C;Superfamily: mouse mast cell factor
C;Superfamily: mouse mast cell factor
C;Superfa
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                                                                                                               - quail
                                                                                                stem cell factor long form precursor
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RESULT 15
A35971
mast call growth factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A35971
R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R.; Milliams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R.; Milliams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R.; A;Reference number: A35971; MulD:91004215; PMID:1698553
A;Retus: preliminary
A;Molecule type: protein
A;Residues: 1-49 *MIL.
A;Residues: 1-49 *WIL.
A;Residues: UNIPROT:P20826; UNIPARC:UP10000179561
C;Superfamily: mouse mast cell growth factor
C;Reywords: transmembrane protein
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5
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16.3%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 2.6e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3;
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Search completed: February 22, 2006, 18:20:26 Job time : 19:1901 secs

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5.1.7
Biocceleration Ltd
version 5
GenCore (c) 1993
        Copyright
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sw model - protein search, using OM protein

Pebruary 22, 2006, 18:05:51 ; Search time 107.152 Seconds
(without alignments)
1369.555 Million cell updates/sec Run on:

US-10-620-642-46 1061 Title: Perfect score:

1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKYIYLI 208 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 segs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	3 homo sapien	felis	0 sus scrofa	-	4 papio cynoc	-		.9 capra hircu			.8 mustela vis	EUM	_	_	.9 macaca mula	2 homo sapien	4 rattus norv			8 gallus gall	4 mus musculu		ambystom	xenobns		• •	6 brachydanio				2 plasmodium
	9803	P21583	P79169	029030	Q95md2	Q865z4	P79368	028132	Q95m19	006220	P21581	095n18	064384	Q78ed8	P20826	086419	Q68dz2	Q54a14	Q7m4n8	090314	009108	061854	Q8c9k1	09ygp2	072XV0	<u>0</u> 8ayn7	Q6dtw3	0 56jh6	0481a5	056jh 5	3i fr	Овшмр2
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	a	SCF	SCF	SCF	SCP	980	SCF	SCP	SCP	SCF CANPA	SCF	SCF_MUSVI	0643	078E	SCF	0864	06BI	0547	O7M4	SCF	SCF_CHICK	0618	280	09YC	072	Q8AYN7_XENLA	060	056.	0431	056.	981	OBM
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*	Query	97.1	85.6	84.8	84.7	83.9	83.8	83.6	83.5	81.3	81.1	81.0	80.6	80.6	80.6	78.7	75.8	68.0	54.3	53.8	53.0	48.0	45.2	30.8	28.2	25.8	25.5	17.3	14.0	11.7	11.0	11.0
	Score	1030	908.5	899.5	898.5	890	889.5	886.5	885.5	862.5	861	859.5	855	855	855	835	804	721	576.5	570.5	562.5	509	480	327	299.5	273.5	270.5	184	149	124	116.5	116.5
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lum lum lum jum gla gla gla sma lla lla lla sma sma
plasmodium plasmodium plasmodium clover yell candida gla dictyostell caenorhabdi ashbya goss ureaplasma emericella emericella rickettsia vibrio para
QBmwp1 QBmwh2 QBwh2 Q64047 Q64143 Q15458 Q15678 Q15678 Q9646 Q9646 Q9646 Q9646 Q967834 Q87834
QBWWP1_PLAFA QBWH2_PLAFA QGFA77_PLARE QGFLY9_CANGA QGFLY9_CANGA QGFLY9_CANGA QGFYG_EBL Q19545_CAEEL Q19545_CAEEL Q19578_ASHGO Q9PQJ8_UREPA Q9PQJ8_UREPA Q9PWG_EMENI SCA4_RICPE Q9PW34_VIBPA Q6FV48_CANGA
N N H N N N N N N N N N N N N N
1713 1716 1665 3072 1011 1490 1447 1498 1039 251
0.00 4.00 9.00
1116.5 116.5 116.5 106.5 97.5 97.5 96.5 96.5 95.9
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ALIGNMENTS

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[3]

WUCLEOTIDE SEQUENCE (ISOFORM 2).

MUCLEOTIDE SEQUENCE (ISOFORM 2).

MEDLINE=99160429; PubMed=10049787; DOI=10.1006/bbrc.1999.0260;

Blair H.C., Julian B.A., Cao X., Jordan S.E., Dong S.S.;

"Parathyroid hormone-regulated production of stem cell factor in human osteoblasts and osteoblast-like cells.";

Biochem. Biophys. Res. Commun. 255:778-784(1999).
                                                              December 2014 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name-KITLG; Synonyms-MGF, SCF;
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
MATTIN F.H., SuggB S.V., Langley K.B., Lu H.S., Ting J., Okino K.H.,
Morris C.P., McNiece I.K., Jacobsen P.W., Mendiaz B.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher B.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
Poppe J.A., Leelle I., Wen D., Lin C.-H., Cupples R.L., Zeebo K.M.;
Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE [LARGE SCALE MENNA] (ISOFORM 1).
NUCLECTIDE SEQUENCE [LARGE SCALE MENNA] (ISOFORM 1).
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTION SEQUENCE (ISOFORM 2).

PubMed=1724381;

Nulliams D.E., Tushinski R., Gimpel S., Eisenman J.,

Cannizzaro L.A., Aronson M., Croce C.M., Huebner K., Cosman D.;

"Alternate splicing of mRNAs encoding human mast cell growth factor
and localization of the gene to chromosome 12q22-q24.";

cell Growth Differ. 2:373-378 (1991).
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Volume SEQUENCE.

Han C., Peng X., Yuan J., Qiang B.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                       273 AA
                                           PRT;
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell factor DNAs.";
Cell 63:203-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                           HUMAN
SCP HUMAN

ACC HANAN

DT 01-MA

DE CSC HA

DE CSC HA

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DE CSC HA

DE CALL

CO OC MAMBOLI

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RA CALL

RA CALL

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RA ANGER

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similarity).

-I-ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=SCF246;
IsoId=P21583-1; Sequence=Displayed;
Name=2; Synonyms=SCF220;
IsoId=P21583-2; Sequence=VSP 006022;
-I-DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-I-DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-I-DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-I-DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-I-DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-I-DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-I-DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/WGFID142.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WUCLECTIDE SEQUENCE OF 167-248 (ISOFORM 2).

MUCLECTIDE SEQUENCE OF 167-248 (ISOFORM 2).

MEDLINE=92360843; PubMed=1379846;

TOYOCA M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;

TOYOCA M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;

Toyoca M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;

Toyoca M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;

Int. J. Hematol 55:301-304(1992).

Int. J. Hematol 67:301-304(1992).

Int. J. Hematol 
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan R.J., McKernan R.J., Male V. Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Mazny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmin J.B., Schmitz J., Myers R.M., Sphnerch A., Schein J.B., Sones S.J.M., Marra M.A., Schein J.B., Jones S. J.M., Marra M.A., Schein J.B., Jones S.J.M., Marra M.A., Schein J.B., Jones J.B., Jones J.M., Jones J.B., Jones J.M., J
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GO: GO:0005173; F:stem cell factor receptor binding; NAS.
GO: GO:0008173; F:stem cell factor receptor binding; NAS.
GO: GO:0001839; P:cell proliferation; TAS.
GO: GO:0007165; P:signal transduction; TAS.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTHAL1574; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."; . Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; AF119835; AAAD22048.1; -; mENA.

EMBL; AF400437; AAX92485.1; -; mENA.

EMBL; BF400437; AAX92486.1; -; mENA.

EMBL; BC069733; AAH65733.1; -; mENA.

EMBL; BC069783; AAH65793.1; -; mENA.

EMBL; BC069797; AAH6773.1; -; mENA.

EMBL; BC06777; AAH67797.1; -; mENA.

EMBL; A3597; AAH7725.1; -; mENA.

PIR; B61190; B61190.

PIR; BRANA.

PIR; B61190; B61190.

PIR; B
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
11-MAY-2005 (Rel. 47, Last annotation update)
12-MAH-2005 (Rel. 47, Last annotation update)
13-MAH-2015 (MGF).
14-MAH-2015 (MGF).
15-MAH-2015 (GAL).
15-MAH-20
                                                                                                   Kit ligand.

Extracellular (Potential).

Potential.

Cycplasmic (Potential).

N-linked (GLONAC. ..) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.
3D-structure; Alternative splicing; Cell adhesion; Glycoprotein;
Growth factor; Signal; Transmembrane.
SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTIGACSP 006022.

55 5 L -> S (in Ref. 3 and 4; AAK92486)

128 124 K -> R (in Ref. 3 and 4; AAK92486)

134 134 L -> F (in Ref. 3 and 4; AAK92486)

273 AA; 30899 MW; 19FD362CB59C6607 CRC64;
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NCBI_TaxID=9685;
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215
215
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118
195
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P79169;
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TOPO DOM
CARBOHYD
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CARBOHYD
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DT 28-FE
DT 10-MA
DE Kit 1
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CO Felin

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RC TISSUESTELE SUCCESSORY TO THE STRUCTURE MEDIATES AND CC caugment the proliferation of both myeloid and lymphoid cc cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

CC -: SUBGNIT: Homodimer, non-covalently linked (Probable).

CC -: SUBGNIT: Homodimer, non-covalently linked (Probable).

CC -: SUBGNIT: A soluble form (By similarity).

CC -: PTM: A soluble form (By similarity).

CC -: PTM: A soluble form (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61 MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECHERFF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWIITCIYLQLLLFNPLVRTQGICRNRVTDDVKDVKLVANLPKDYKITLKYVPG 60
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kit ligand.
Extracellular (Potential).
Botential.
Cytoplasmic (Potential).
N-linked (GloNAc. ..) (Pot
Sysimilarity.
By similarity.
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PF3C87114D7BA6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the SCF family.
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Matches 176; Conservative
                                                                  [1]
NUCLEOTIDE SEQUENCE
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(29930).
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyms=MGF;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
(Sytoplasmic (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
By similarity.
By similarity.
By similarity.
                                                                                                       -1- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
85.6%; Score svo.3; 22., Best Local Similarity 88.2%; Pred. No. 5.2e-62;
Matches 180; Conservative 13; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_006021.
C5B78DB4791237BB CRC64;
                              Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                           IsoId=P79169-2; Sequence=VSP_006021;
                                                       IsoId=P79169-1; Sequence=Displayed;
Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform 2)
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similarity).
ALTERNATIVE PRODUCTS:
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DISULFID
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SCP_PIG
ID SCF
DT 01-
DT 01-
DT 10-
DB Kit
DB Kit
CB Nam
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CONFLICT
CARBOHYD
DISULPID
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                                                          DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCF HORSE STANDARD; PRT; 274 AA.

Q95MD2; O62765; Q95MG3; Q95MG8; Q9N1Y5;
28-FRB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).

Name=KITLG; Synonyms=MGF, SCF;
Equus caballus (Horse).
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin;
Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
"An equine sequence homologous to stem cell factor (KIT-ligand).";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Terry R.R., Bailey E.F., Cothran E.G.; "Evaluation of MGF as the candidate gene for Appaloosa spotting."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor; Signal; Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Cothran E.G., Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 4-264.
Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Br
"Equus caballus mast cell growth factor (MGF).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kit ligand.
Extracellular (Potential)
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Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (F. N-linked (Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 107-202 AND 227-274.
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EMBL; AF053498; AAC97076.1; -; mRNA.
EMBL; AF367704; AAK63249.1; -; Genomic_DNA.
EMBL; AF367706; AAK63250.1; -; Genomic_DNA.
EMBL; AF130770; AAF36716.1; -; Genomic_DNA.
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InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
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PANTHER; PTHR11574; SCF; 1.
Pfam; PPC43404; SCF; 1.
Cell adhesion; Glycoprotein;
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SCP HORSE
JD 5675 H
JD 5675 H
JD 5675 H
JD 5675 H
JD 28-PE
DT 10-NB
DE Kit 1
RN NUCLE
RN NUCLE
RN TELTY
RN TELT
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                         7;
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    . .) (Potential)
                                                                                                                                                             DB 1; Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WUCLEOTIDE SEQUENCE.
Stalina T., Storek J.;
Stalina T., Storek J.;
Stalina T., Storek J.;
Submitted (IAM-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY226584; AA072537.1; -; mRNA.
EMSP; P21583; 18X2.
SNR; 086524; 29-161.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005173; F:erem call factor receptor binding; IEA.
GO; GO:0007155; F:cell adhesion; IEA.
                                                                                                                                                                                                       11; Indels
N-linked (GlcNAc. ..) (Pot
By similarity.
By similarity.
Q -> P (in Ref. 2).
Missing (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 AA; 27887 MW; 937B3CAF28D694FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              036524 PRIM PRELIMINARY; PRT; 245 AA. 086524. Cont. 1017. 203 (TrEMBLrel. 24, Created) 01-UTM-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                          84.7%; Score 898.5; DB 1
86.8%; Pred. No. 3.1e-61;
iive 15; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TKPFMLPPVAASSLRNDSSSSNRK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 TKPFMLPPVAASSLRNDSSSSNSK 203
  207 207 N-:
29 114 BY
68 164 BY
15 15 Q 1
241 241 Mi
274 AA; 31217 MW;
                                                                                                                                                                                                       Matches 177; Conservative
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15; Mismatches 13; Indels

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Matches 175; Conservative
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SCF BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOKINE 11:249-256 (1999).

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (89 similarity).
-!- SUBCELLUIAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (89 similarity).
-!- PTM: A soluble form (89 similarity).
                  SUF SHEEP STANDARD; PRT; 267 AA.

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCP) (Mast cell growth factor) (MGP) (Fragment).

Name-KITLG; Synonyms-SCF;
Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Pecora; Bovidae; Caprinae; Ovis.

Novida States (Sheep).

Novidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                  TISSUE-Ovarian follicle,
MEDLINE-96413880; PubMed-8662240; DOI=10.1007/8003359900142;
Tisdall D.J., Quirke L.D., Galloway S.M.;
"Ovine stem cell factor gene is located within a syntenic group on chromosome 3 conserved across mammalian species.";
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99263397; PubMed=10328863; DOI=10.1006/cyto.1998.0430; MCINGE C.J., Deane D., Thomson J., Broad A., Haig D.M.; MThe cloning and expression of the cobx for ovine stem cell factor (kit-ligand) and characterization of its in vitro haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor; Signal; Transmembrane
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Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
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Extracellular (Potential).
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             267 AA
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SNR; P79368; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
Ffan; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth fac
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ЕМВL; Z50743; CAA90620.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                  Mamm. Genome 7:472-473 (1996).
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE OF 8-267.
                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 1-202
             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity."
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SEQUENCE
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Length 267;

Score 889.5; DB 1; Pred. No. 1.5e-60;

83.8%;

Best Local Similarity

Query Match

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028132; O9TU74;
28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITIG; Synonyms=SCF;
Name=KITIG; Synonyms=SCF;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;
Mammalia; Eutheria, Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.2):
                                                                              MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                        ENVKKSSKSPEPRQFTPEKKFFGIFNKSIDAFKDLEIVASTMSECVISSTSSPEKDSRVSV 180
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MEDLINE=931531; PubMed=10384045; DOI=10.1007/8003359901076;

A REDLINE=931531; PubMed=10384045; DOI=10.1007/8003359901076;

Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;

The missense mutation in the bovine MGF gene is associated with the roan phenotype in Belgian Blue and Shorthorn cattle.";

Mamm. Genome 10.710-712(1999).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-I- SUBINIT: Homodimer, non-covalently linked (Probable).

-I- SUBINIT: Homodimer, non-covalently linked (Probable).

-I- SUBINIT: Homodimer, non-covalently linked (Brobable).

-I- SUBCELLULAR ALCAPION: Type I membrane protein (1soforms 1 and 2): "Similarity).
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                                                                                                    61 MDVLPSHCWISEMVEQLSVSLTDLLDKPSNISEGLSNYSIIDKLVKIVDDLVECMEEHSP
               MKKTQTWILTCIYLQLLLPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV
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MEDLINE-94319176; PubMed=7520283; DOI=10.1016/0167-4889(94)90084-1;
Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
"Cloning and characterization of cDNAs encoding two normal isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2;
IsoId=Q28132-2; Sequence=VSP 006020;
PTM: A soluble form is produced by proteolytic processing of
isoform 1 in the extracellular domain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bovine counterpart of stem cell factor.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [3]
NUCLEOTIDE SEQUENCE OF 204-239, AND VARIANT ASP-218.
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                                                                                                                                                                                                                                                                                                                                                                                                   274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bovine stem cell factor.";
Biochim. Biophys. Acta 1223:148-150(1994)
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NCBI TaxID=9913;
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                                                                    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its
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                                                                                        the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYCIIDKLVKIVDDLVBCWEEHSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOF-VVASETSDCVVSSTLSPEKDSRVSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYMORPHISM: The roan locus is responsible for the coat coloration of Belgian Blue and Shorthorn cattle. The solid-colored and white animals are homozygotes, and the roan animals, with intermingled colored and white hairs, are heterozygous. The roan phenotype is due to the Asp-218 mutation. SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                   (in
                                                                                                                                                                                                                                             SCF CAPHI STANDARD; PRT; 274 AA.
095M19;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mass cell growth factor) (MGF).
Name=KTILG; Synonyms=SCF;
Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                             adhesion, Glycoprotein; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
                                                                                                                                                                                                                                                                                                                                                             isoform 2).
/FIId=VSP_006020.
A -> D (in roan allele).
D6C1DDB77B0CB12B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                               83.6%; Score 886.5; DB 1
85.3%; Pred. No. 2.6e-60;
                                                                                                                                           EMBL; AB033716; BAA94808.1; -; mRNA.
EMBL; AR120154; AAD55355.1; -; Genomic_DNA.
PIR; S47571; S47571.
SMR; Q28132; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; SCF;
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Alternative spliting; Cell adhesion; Glycopro Polymorphism; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.3%; Pred. No. 2.6e-
Matches 174; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKPFMLPPVAASSLRNDSSSSNSK 203
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274 AA;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kit ligand.

Bxtracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlanAc. .) (Potential).

N-linked (GlanAc. .) (Potential).

N-linked (GlanAc. .) (Potential).

By similarity.

By similarity.
                                                                                                                                                                                                                                                                                                                                -!- PTM: A soluble form is produced by proteolytic processing of extracellular domain (By similarity).
Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%; Score 885.5; DB 1; Length 274; 85.3%; Pred. No. 3.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity.
BBFE669A509EF65D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB002152; BAB71753.1; -; mRNA. SMR; Q95M19; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF: 1.
PÉam; PF02404; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential
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                 Pecora; Bovidae; Caprinae; Capra.
NCBI_raxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 By
31053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 174; Conservative
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238
274
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26 25
26 25
216 22
239 2
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97 145
1145 11
196 11
274 AA;
                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q06220; Q8SPM6;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KKTLG; Synonyms=MGF;
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor; Signal; Transmembrane.
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(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                         Martin F.H.; "Canine stem cell factor (c-kil ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture."; Exp. Hematol. 20:1118-1124(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 274;
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Kit ligand.

Forential.

Cytoplasmic (Potential).

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Poten N-linked (GlCNAc. .) (Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%; Score 862.5; DB 1; Length 84.8%; Pred. No. 1.8e-58; ive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4182BE9AED00793B CRC64;
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EMBL; AX094361; AAM16280.1; -; mRNA.

PIR; 146929; 146629.

SMR; Q06220; 29-161.

SMR; Q06220; 29-161.

InterPro; IPRO12351; Cytokine 4 hlx.

InterPro; IPRO3452; SCF.
  274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93106145; PubMed=1281786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 17-274.
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Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted soluble form.
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Best Local Similarity 84.84
Matches 173; Conservative
STANDARD;
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196
29
68
274 AA;
                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                         TISSUE=T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Tail:
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61 MDVLPSHCWISVMVBQLSVSLTDLLDKPSNISBGLSNYSIIDKLVKIVDDLVECTBGYSF 120
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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PROTEIN SEQUENCE OF 26-190, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.

NUCLECTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.

MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;

Martin F.H., Sugge S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,

Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,

Smith K.A., Johnson M.J., Parker V.P., Plores J.C., Patel A.C.,

Fisher B.F., Erjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,

Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;

Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 63:195-201(1990). Provide the proliferation of mast cells. Able to PUNCTION: Stimulates the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 26-39.
MEDLINE=91004218; PubMed=2208278; DOI=10.1016/0092-8674(90)90300-4; Zaebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A., Karkare S. B., Sachdev R.K., Yuschenkoff V.N., Birkett N.C., Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz B.A., Langley K.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Buffalo; TISSUE-Liver;
MEDLINE=91217037; PubMed=1708771;
MI H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
Mendiaz E.A., Zsebo K.M., Langley K.E.;
"Amino acid sequence and post-translational modification of stem cfactor isolated from buffalo rat liver cell-conditioned medium.";
J. Biol. Chem. 266:8102-8107(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification, purification, and biological characterization of hematopoletic stem cell factor from buffalo rat liver-conditioned medium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MX-1991 (Rel. 18, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-MX-2005 (Rel. 47, Last annotation update)
kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF)
cell growth factor) (MGF) (Hematopoietic growth factor KL).
Name=Kitlg; Synonyms=Mgf;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teramoto T., Nagashima M., Thorgeirsson S.S.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                              273 AA
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                                                                                                                                                                                                                                                                                   181 TKPFMLPPVAASSLRNDSSSSNRK 204
                                                                                                                                                                                                                                                          180 TKPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                P21581; Q9QWZ4; Q9Z2E7;
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Mustelinae; Mustela.
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90
97
                                                                                Q95N18; Q95MN5;
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                                                                 SCF MUSVI
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                                       RESULT 11
SCF MUSVI
                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOLKKSPKSPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
probably interleukins.
SUBUNT: Homodimer, non-covalently linked (Probable).
SUBCELLUIAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (in
                                                                                                                                     ISOIG-P21561-2; Sequence-VSP 006025; ISOIG-P21561-2; Sequence-VSP 006025; DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis. PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain. SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                       EMBL; AF071204; AAD02827.1; -; mRNA.
EMBL; AF071205; AAD02828.1; -; mRNA.
FNBL; MS9966; AAA42117.1; -; mRNA.
FNBL; MS9966; AAA42117.1; -; mRNA.
FNBL; MS9966; AAA42117.1; -; mRNA.
SMR; P21581; 29-159.
SMR; P21581; 29-159.
ENSEMD!; ENSRNOG00000005386; Rattus norvegicus.
InterPro; IPR012351; Cytokine_4-hlx.
InterPro; IPR012351; Cytokine_4-hlx.
InterPro; IPR013415; SCF.
PANTHER; PTHR11574; SCF; 1.
Alexinative splicing; Cell adhesion; Direct protein sequencing;
Glycoprotein; Growth factor; Pyrrolidone carboxylic acid; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
Cytoplasmic (Potential).
Pyrrolidome carboxylic acid.
Pyrrolidome carboxylic acid.
N-linked (GlcNAc. .); partial.
O-linked (Probable).
O-linked (Probable).
O-linked (Probable).
N-linked (GlcNAc. .); partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.1%; Score 861; DB 1; Length 273; 82.3%; Pred. No. 2.4e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoform 2).
/FrId=VSP_006025.
S -> P (in Ref. 1; AAD02828).
COF56527DC93FD27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kit ligand.
Extracellular (Potential)
                                                             similarity/
bull remoders:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
                                                                                                Name=1; Synonyms=KL-1;
IsoId=P21581-1; Sequence=Displayed;
Name=2; Synonyms=KL-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30712 MW;
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Matches 167; Conservative
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1168
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273 AA;
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218
238
26
90
                                                         similarity)
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TRANSMEM
TOPO DOM
MOD RES
CARBOHYD
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181 KPFMLPPVAASSLRNDSSSSNRK 203
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                             Mustela vison (American mink).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Mustelidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform 2).
/FIId=VSP_006024.
5 -> P (in Ref. 1; AAK73366).
5 -> N (in Ref. 1; AAK73366).
EREPOBY -> RESFEKRUNGFYHTVLSYLGG (in Ref. 1; AAK73366).
                                                                                                                                                                                                                      Bennett R.D., Murphy B.D.;
Submitted (Nov-2000) to the EMBL/GenBank/DDBJ databases.

-!- KUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoidtic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!- SUBUNIT: Homodimer, non-covalenty linked (Probable).
-!- SUBUNIT: Homodimer, non-covalenty linked exists as a secreted soluble form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
in
                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (Crit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyme=SCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adhesion; Glycoprotein; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kit ligand.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
Cytoplasmic (Potential).
N-linked (GlCNAc. . . ) (P
N-linked (GlCNAc. . . ) (F
                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity.
274 AA
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                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMR; Q95N18; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY013712; AAG37434.1; -; mRNA.
EMBL; AF323757; AAK73366.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PANTHER; PTHR11574; SCF; 1. Pfan; PPO2404; SCF; 1. Alternative splicing; Cell adh. Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                       -1- ALTERNATIVE PRODUCTS
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
171
274
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171
268
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61 MDVLPSHCWLRDMVIQLSLSLTTLLDKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91160046; PubMed=1705866; DOI=10.1016/0092-8674(91)90326-T; Planagan J.G., Chan D.C., Leder P.; Tannemenbrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Sld mutant."; Cell 64:1025-1035(1991).

RMBL, M64262; AAA39378.1; -; mRNA.

SMR; Q78E08; 29-159.

MG1; MG1:96974; Kitl.

MG7; MG1:96974; Kitl.

MG7; G0:0005515; C:extracellular space; IDA.

G0; G0:0005515; C:extracellular space; IDA.

G0; G0:0005515; F:protein binding; IDA.

G0; G0:0005181; P:grem cell factor receptor binding; IDA.

G0; G0:0005181; P:grem cell development; TAS.

G0; G0:000731; P:grem cell development; TAS.

G0; G0:000731; P:grem cell development; TAS.

G0; G0:000731; P:grem cell development; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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Mus musculus (Mouse).
Eukaryota; Meteazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
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KL) (Steel
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82.3%; Pred. No. 5e-58;
ive 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCF MOUSE STANDARD; PRT; 273 AA.
P20826; P97332; Q62524; Q64222; Q921N5;
01-FRB-1991 (Rel. 17, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor)
cell growth factor) (MGF) (Hematopoietic growth factor 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23222 MW; C74DD639566EB817 CRC64;
                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                        Z
                                                                                                                                                                                                        208
        181 KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 105-JUL-2004 (TrEMBLrel. 27, 11, 11gand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003452; SCF. Pfam; PF02404; SCF; 1.
                                                                                                                                                                                                Q78ED8 MOUSE PRELIMINARY;
Q78ED8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 82.3
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02404; SCF; 1
SEQUENCE 208 AA; 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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AC SCF_M
AC SCF_M
DT 01-FB
DT 10-MA
DE Kit 1
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DE CE11
DE CE11
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OS NAME M
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                                                                                                                                                                                                                                                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKDSRVSV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDVLPSHCWLRDMVIQLSLSLTTLLDKFSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
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                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                  1 MKKTQTWIITCIYLQLLLFNPLVRTKGICRNRVTDDVKDVTKLVANLPKDYKIALNYVPG 60
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MEDLINE-92330001; PubMed=1378327;

MEDLINE-92330001; PubMed=1378327;

MEDLINE-92330001; PubMed=1378327;

MEDLINE-92330001; PubMed=1378327;

MEDLINE-92330001; PubMed=1378327;

MIDLINE-92330001; PubMed=1378327;

MIDLINE-92330001; PubMed=1378327;

MIDLINE-92330001; MIDLINE-92;

MIDLINE-92330001; MIDLINE-92;

MIDLINE-92330001; MIDLINE-93; MIDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTOTWILTCIYLOLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                               Gaps
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0
                                                                                 Length 274;
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80.6%; Score 855; DB 2; Length 208;
Best Local Similarity 82.3%; Pred. No. 5e-58;
Matches 167; Conservative 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    064384;
064384;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-2996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
C-kit ligand C-terminally truncated secreted form KL-Sld.
                                                                                                                                                           Indels
31035 MW; 5AC1619014AE5E72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02404; SCF; 1.
SEQUENCE 208 AA; 23222 MW; C74DD639566EBB17 CRC64;
                                                                     Query Match 81.0%; Score 859.5; DB 1; Best Local Similarity 83.3%; Pred. No. 3.1e-58; Matches 170; Conservative 16; Mismatches 17;
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SEQUENCE
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63:213-224 (1990).
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

STRAIN=C57BL/6J; TISSUB=Cerebellum;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

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Nagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

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Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
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transversion or an insertion.";
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Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.;
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defect in the steel factor cytoplasmic tail.";
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                                                                MEDLINE-91004223; PubMed=1698558; DOI=10.1016/0092-8674(90)90304-W; Anderson D.M., Lyman S.D., Balrd A., Wignall J.M., Eisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS SER-122, PRO-193 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207 STRAIN=C3H/E1; TISSUE-Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
MEDLINE=97002551; Pubmed=8849898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE (ISOFORM 1).
                                           NUCLEOTIDE SEQUENCE (ISOFORM 1).
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phenotype.";
Mutat. Res. 382:75-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=102/E1 x C3H/E1;
                                                                                                                                                         Cell 63:235-243(1990).
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Rambolina R., Mank K., Kawa Y., Rambolina R., Rambolina R.,
Rambolina R., Mank K., Kawa Y., Rambolina R., Mank R., Sako R.,
Rambolina R., Caeberg B., Loulina P.S., Wanger L., Shemen C.K., Schular G.D.,
Rambolina R., Mandolina P.S., Wanger L., Shemen C.K., Schular G.D.,
Rambolina R., Mandolina W., Moore T., Mang J., Hayds R.A.,
Rambolina R., Varbusha R., Moore T., Mang J., Hayds R.A.,
Rambolina R., Mandolina W., Moore T., Mang J., Mangolina R.,
Rambolina R., Mandolina W., Mangolina R., Mangolina R.,
Rambolina R., Mandolina R., Mangolina R., Mangolina R.,
Rambolina R., Mandolina R., Mangolina R., Mangolina R.,
Rambolina R., Mangolina R.,
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PARTIAL PROTEIN SEQUENCE OF 26-78.

MEDLINE=91004215; PubMed=169853; DOI=10.1016/0092-8674(90)90297-R; Williams D.E., Elsenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.; Tadentification of a ligand for the c-kit proto-oncogene."; Cell 63:167-174(1990).

--- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.

--- SUBGINIT: Homodimer. non-covalently linked (Probable).

--- SUBCELLULAR LOCATION: Type I membrane protein (1soforms 1 and 2). Also, exists as a secreted soluble form (1soform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=XL-1;
Isold=P20826-1; Sequence=Displayed;
Name=2; Synonyms=KL-2;
Isold=P20826-2; Sequence=VSP 006023;
-!- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-!- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
-!- SIMILARITY: Belongs to the SCF family.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
SCF (Fragment).
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M59915; AAA40095.1; -; mRNA.
EMBL; M57647; AAA39538 1; -; mRNA.
EMBL; S60534; ABA22555.2; -; mRNA.
EMBL; X68989; CAA48778.1; -; mRNA.
EMBL; U44724; -; NOT ANNOTATED CDS; Genomic_DNA.
EMBL; U44725; AAC$2447.1; -; mRNA.
EMBL; X95381; CAA464667.1; -; mRNA.
EMBL; X99322; CAA64667.1; -; mRNA.
EMBL; X99322; CAA676598.1; -; mRNA.
EMBL; X10287; CAA71329.1; -; mRNA.
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Q864L9;
                                                                                                                                                                                                                                           similarity).
ALTERNATIVE PRODUCTS:
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Q864L9 MAC
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86 DKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSPKSPEPRLFTPEEFPRIFN 145
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                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Cercopithecidae, Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                               R EMEL; A7247403; AAP03067.1; -; mRNA.

R HSSP; P21583; 1SCF.

R GG1, G0:0016020; C:membrane; IEA.

GG3; G0:0005173; F:stem cell factor receptor binding; IEA.

R GO; G0:0005175; P:stem cell factor receptor binding; IEA.

R GO; G0:0007155; P:cell adhesion; IEA.

R ITRN03452; SCF.

R Pfam; PP02404; SCF; 1.

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I SEQÜENCE 164 AA; 18430 MW; 6AFE3A568730110D CRC64;
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NUCLEOTIDE SEQUENCE.
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February 22, 2006, 18:19:42; Search time 25.2121 Seconds (without alignments) 682.074 Million cell updates/sec
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                                                                                                                                                                                                                                                                                1 MKKTQTWILTCIYLQLLFN......AASSLRNDSSSSNSKYIYLI 208
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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US-09-224-681-46
US-09-625-251-46
US-09-625-251-46
US-09-224-683-46
US-08-20-378-2
US-08-428-9
US-08-428-9
US-08-428-9
US-08-482-918-48
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US-09-224-681-49
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ALIGNMENTS

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WESULY.

US-08-816-252A-6

Sequence 6, Application US/08836252A

Sequence 6, Application US/08836252A

Patent No. 617556

GENERAL INFORMATION:

APPLICANT: Sharkey, Andrew M.

APPLICANT: Sharkey, Andrew M.

APPLICANT: Sharkey, Andrew M.

APPLICANT: SEQUENCES: 18

CORRESPONDENCE ADDRESS: 18

CORRESPONDENCE ADDRESS: 18

CORRESPONDENCE ADDRESS: 18

CONTEST: 1100 NEW YORK AVENUE, N.W. SUITE 600

CITT: WASHINGTON

STATE: 0.C.

CONTYRY: USA

ILLY WASHINGTON

COMPUTER: FLODBY disk

COMPUTER: Ploppy disk

COM
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GENERAL INOCRAPATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Boseslam, Robert M.
APPLICANT: Boseslam, Rethod for Enhancing the Efficiency of Gene TITLE OF INVERTION: Transfer with Stem Cell Factor (SCF) Polypeptide CORRESPONDENCE ADDRESSES: Marshall, O'TOole, Geretein, Murray & Borun ALDRESSES: Marshall FORM: AND Geretein County Compaction of COUNTY: United States of America COUNTY: APPLICATION NUMBER: 09/005, 893
FILING DATE: 24-MAY-1995
FILING DATE: 24-MAY-1995
FILING DATE: 24-MAY-1995
FILING DATE: 24-MAY-1990
FILING DATE: 11-UNI-1990
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                    MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDXLVNIVDDLVECVKENSS 120
                                                                                                                                  KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEFRONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                    181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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Sequence 46, Application US/08482918

Patent No. 6207417

GENERAL INPORMATION:

APPLICANT: Zeebo, Krisztina M.
APPLICANT: Suggs, Sidney V.

APPLICANT: Bosselman, Robert A.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago

STREET: 6100 Sears Tower, 233 South Wacker Drive CITY: Chicago

STRYE: Illingis

COUNTRY: United States of America

ZIP: 60666-6402

COMPUTER: IBM FC compatible

COUNTRY: TIM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURSSIFICATION NUMBER: US/08/482,918

FILING DATE: 07-UNN-1995

CITAGNEY/AGENT INPERMATION: ATTORNEY/AGENT INPERMATION

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107
                                               Query Match 100.0%; Score 1061; DB 2; Length 208; Best Local Similarity 100.0%; Pred. No. 3.4e-101; Matches 208; Conservative 0; Mismatches 0; Indels 0.
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Best Local Similarity 100.0%; Pred. No. 3.4e-101;
Matches 208; Conservative 0; Mismatches 0;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
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TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-728A-46
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US-03-36-728A-46
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Best Local Similarity 100.0%; Pred. No. 3.4e-101;
Matches 208; Conservative 0; Mismatches 0;
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE SCHRARGINGS:
LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                         ; TOPOLOGY: linear
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US-09-224-681-46
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1 Sequence 46, Application US/09224683

1 Patent No. 6841147

2 GENERAL INFORMATION:

APPLICANT: Zeebo, Krisztina M.

APPLICANT: Zeebo, Krisztina M.

APPLICANT: Suggs, Sidney V.

APPLICANT: Buggs, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6310 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

CONPUTRY: United States of America

ZIP: 60606-6402

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Ploppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1061; DB 2; Length 208; Best Local Similarity 100.0%; Pred. No. 3.4e-101; Matches 208; Conservative 0; Mismatches 0; Indels 0
## APPLICATION NUMBER: 07/573,616
## PILING DATE: 24-AUG-1990
## PELICATION NUMBER: 07/57,198
## PELICATION NUMBER: 07/422,383
## PELICATION NUMBER: 07/422,383
## PELICATION NUMBER: 07/422,383
## ATTONIEY/AGENT INFORMATION:
## REFERENCE/DOCKET NUMBER: 01017/32957A
## TELECOMMUNICATION INFORMATION:
## TELECOMMUNICATION INFORMATION:
## TELEFRA: 01017/32957A
## TELEFRA: 0107/474-0448
## TELEFRA: 0107/474-044
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121 KOLKKSFKSPEPRLFTPEEFPRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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; Sequence 9, Application US/08628428
; Sequence 9, Application US/08628428
; Patent No. 5885562
; TITLE OF INVENTION:
; APPLICANT: Lu, Haieng
TITLE OF INVENTION:
; APPLICANT: Lu, Haieng
; TITLE OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
; STREET: 1840 Delavilland Drive
CITY: Thousand Oaks
; STATE: CA
COUNTRY: USA
; CONTRY: THOUSAND Oaks
; CONPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; COMPUTER: TEM PC compatible
; COMPUTER: PLOPPY disk
; COMPUTER: TEM PC compatible
; COMPUTER: PLOPPY disk
; CURRENT APPLICATION DATA:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
                               New York
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KPFMLPPVAASSLRNDSSSSNSK 203
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NAME: Haley IT, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cytch
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFRA: 212-596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acids
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                               STATE: N. COUNTRY:
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                                       COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/604,325A

FILING DATE: 17-Jun-2002

APPLICATION NUMBER: 07/982,255

RILING DATE: 25-NOV-1992

APPLICATION NUMBER: 07/539,616

FILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/53,616

FILING DATE: 16-OCT-1990

APPLICATION NUMBER: 07/537,198

FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 36,107

REGISTRATION NUMBER: 312/474-6300

TELECOMMUNICATION INFORMATION:

REGISTRATION INFORMATION:

REGISTRATION INFORMATION:

REGISTRATION NUMBER: 312/474-6300

TELEBEPAX: 312/474-6300
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APPLICANT: No. 55.5708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
STATE: Illinois
COUNTRY: United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08220379B
Patent No. 5525708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acid
TYPE: amino acid
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US-08-220-379B-2
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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; Sequence 40. Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
APPLICANT: Sabob Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1%; Score 1030; DB 2; Length 273; 99.5%; Pred. No. 7.9e-98; Live 0; Mismatches 1; Indels
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                           REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-0448
TELEFA: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01017/33005
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STATE: 111nois
COUNTY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CIASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 01017/33005
TELEPHONE: 312/474-6300
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Best Local Similarity 99.5'
Matches 202; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-48
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US-08-482-918-49
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1-248 SCF protein begins at amino acid 26; amino acid 1-25
include Met and leader sequences for membrane band form of
recombinant SCF."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTOTWILTCIYLOLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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Sequence 48, Application Marcinal 
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97.1%; Score 1030; DB 1; Length 273;
Best Local Similarity 99.5%; Pred. No. 7.9e-98;
Matches 202; Conservative 0; Mismatches 1; Indels
APPLICATION NUMBER: US/08/628,428
CLASSIPTCATION: 435
CLASSIPTCATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Knight, Matthew W
REGISTRATION NUMBER: 36,846
REGISTRATION NUMBER: 36,846
REGISTRATION NUMBER: 36,846
REGISTRATION NOW 9:
REPRENCE/DOCKET NUMBER: A-400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
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ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
LOCATION: 1..273
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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1 MEKENOTWILTCIYLOLLLENPLYKTEGICRNRYTRNYKOVTKLVANLPKOYMITLKYVPG 60
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                                                                                                                                                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                       121 KOLKKSFKSPERLFTFEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Zeebo, Krisztina M.

APPLICANT: Bosselman. Robert A.

APPLICANT: Bosselman. Robert A.

APPLICANT: Bosselman. Robert A.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: G300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILING DATE:
CLASSIFICATION DATA:
PRICK APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRICK APPLICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/539,616
FILING DATE: 24-AUG-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/533,198
FILING DATE: 11-JUN-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRICK APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1999
ATTONEY/AGRAY INFORMATION:
ANDRENT NUMBER: 07/537,198
FILING DATE: 11-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 01017/35199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: 111,1nois
COUTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KPFMLPPVAASSLRNDSSSSNRK 203
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US-09-224-681-48
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                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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Sequence 61, Application US/08482918

Patent No. 6207417

GENERAL INFORMATION:

APPLICANT: Seebo, Krisztina M.

APPLICANT: Seebo, Krisztina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Busselman, Robert A.

APPLICANT: Busselman, Robert A.

APPLICANT: Busselman, Robert A.

TITLE OF INVENTION: Francis H.

TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCES: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: DEM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

ATTORNEY/ACRIT INFORMATION:

NAME: Clough, David W.

REGESTRATION NUMBER: 35,010

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 273 amino acids
amino acid
                                                              ; TOPOLOGY: 11mea.
; MOLECULE TYPE: protein
US-08-482-918-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-61
                             single
IYPE: amino acid
                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-482-918-61
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Sequence 49, Application US/09224681

Sequence 49, Application US/09224681

Sequence 49, Application US/09224681

Sequence 49, Application US/0924681

Sequence 49, Application US/0924681

Sequence 49, Application US/0924681

APPLICANT: Seabo, Krisztina M.

APPLICANT: Sugges, Sidney V.

APPLICANT: Bosselman, Robert A.

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

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TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

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TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDVLPSHCWISEMVVQLSDSLIDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOPVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 48
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-09-224-681-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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US-09-224-681-49
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Sequence 61, Application US/09224681

Sequence 61, Application US/09224681

Setent No. 6207454

GENERAL INFORMATION:

APPLICANT: Sugge, Sidney V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARBHABIL, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
STATE: Illinois
CONTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: PatentIn Release #1.0, Version #1.30
PRILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FELING DATE: 24-AUG-1990
FRIOR APPLICATION DATA:
FRIING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INPORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
FRECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 499
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-681-49
                                                                                                                                                                                                                                                                                                                                                                             312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.5
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/474-0448
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APPLICATION DATA:

APPLICATION DATA:

CLASSIPICATION
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 09/005,893

FILING DATE: 12-JAN-1998

CLASSIPICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/982,255

FILING DATE: 23-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/989,701

FILING DATE: 01-OCT-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/53,616

FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/53,616

FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/53,616

FILING DATE: 11-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/53,616

FILING DATE: 11-JUN-1990

PRIOR APPLICATION NUMBER: 07/53,616

PRIOR APPLICATION NUMBER: 07/53,616

PRIOR APPLICATION NUMBER: 07/53,616

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/53,616

PRIOR APPLICATION NUMBER: 07/
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 Query Match
 97.1%; Score 1030; DB 2; Length 273;

 Best Local Similarity 99.5%; Pred. No. 7.9e-98;
 1.00 Mismatches 1; Indels 0; Gaps 0;

 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 0; Mismatches 0; Gaps 0;

 Qy
 1 MKKTQTMILTCIYLQLLENPLYKTEGICRNRVTNNVKDVTKLVANLPKDYMILKKVPG 60

 Db
 1 MKTQTMILTCIYLQLLENPLYKTEGICRNRVTNNKDVTKLVANLPKDYMILKKVPG 60

 Db
 61 MDVLSHCWISEMVQLSDSLTDLLDKFSNISEGISNYSIIDKLVNIVDDLVECYKENSS 120

 Ch
 1 MDVLPSHCWISEMVQLSDSLTDLLDKFSNISEGISNYSIIDKLVNIVDDLVECYKENSS 120

Search completed: February 22, 2006, 18:21:58 Job time : 26.2121 secs

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Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
STREET:
STREET:
STREET:
STATE:
STATE
US-10-688-845-87
US-10-620-642-63
US-09-005-234-683-52
US-09-224-688-52
US-09-005-24-68-53
US-09-005-24-68-53
US-09-005-24-68-53
US-09-224-683-53
US-09-224-683-54
US-09-224-683-44
US-10-620-642-44
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US-09-224-683-51
US-09-224-683-51
US-09-224-683-51
US-09-224-683-51
US-09-005-243-51
US-10-620-642-44
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/573,183
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG M:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
    8833339
88333339
881135553333339
881135568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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  February 22, 2006, 18:20:42; Search time 83.0854 Seconds (without alignments) 1046.014 Million cell updates/sec
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1061
1 MKKTQTWILTCIYLQLLLFN......AASSLRNDSSSSNSKXIYLI 208
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*);

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*);
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Biocceleration Ltd
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US-09-005-243-49
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US-09-224-683-49
US-10-175-608-49
US-10-175-608-49
US-10-620-642-49
US-10-620-642-61
US-09-005-243-50
US-09-224-683-50
US-09-224-683-57
US-09-005-243-50
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US-09-005-243-683-57
US-09-005-243-683-57
US-09-224-683-57
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                        version -
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                        GenCore (c) 1993
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seq length: 200000000
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Minimum DB Maximum DB

Database

Result No.

Sequence:

Run on:

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US-10-175-608-46
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                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1061; DB 3; Length 208; Best Local Similarity 100.0%; Pred. No. 7.6e-92; Matches 208; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6060-6402 COUNTRY: United States of America ALP: 6060-6402 COUNTRY: BADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Seebo, Kristina M.

APPLICANT: Sugge, Sidney V.

APPLICANT: Sugge, Sidney V.

APPLICANT: Martin, Francis V.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS: 104

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PAIDR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                 / MOLECULE TYPE: protein US-09-005-243-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-224-683-46
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 11linois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
PRILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35
TELEPHONE: 312/474-6300
TELEFPANE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/10175608
Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 208 amino acids TYPE: amino acids TYPE: amino acid TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-224-683-46
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STATE: Illinois
COUNTRY: United States of America
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LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 208; Conservative
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US-09-005-243-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 XDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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Publication No. US20050080250A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSERE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01017/35199
                                      PELLOR DATE: 09/635,249
PILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/466,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/637,101
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UTN-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UTN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UTN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CLOUGH, DAVIG W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 01017

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEPHONE: 312/474-6448

TELEFAX: 312/474-0448

TELERX: «Unknown»

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERIFITICS:

LENGTH: 208 amino acids

TYPE: amino acid
CLASSIFICATION: <U
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-620-642-46
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180 9 1 MKKTQTWILICIYLQLLLFNPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG 1 MXKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG Gaps ô Length 208; Indels ZIP: 60606-6402
COMPUTER READABLE FOORM:
MEDIUM TYBE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: 100.0%; Score 1061; DB 5; 100.0%; Pred. No. 7.6e-92; tive 0; Mismatches 0; 01017/35199 APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608 APPLICATION NUMBER: 09/635,249
FILING DATE: 16-OCC-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-AUG-2002
APPLICATION NUMBER: 09/466,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 07/982,255
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UDM-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UDM-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UDM-1990
APPLICATION NUMBER: 07/52,383
FILING DATE: 11-UDM-1990
APPLICATION NUMBER: 07/52,383
FILING DATE: 11-DM-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-DM-1990 181 KPFMLPPVAASSLRNDSSSSNSKYIYLI 208 ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 46: US-10-620-642-46

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Sequence 49, Application US/09005243
; Sequence 49, Application US/09005243
; Patent No. US20020018/53A1
GENERAL INPORMATION:
APPLICANT: Seabo, Krisatina M.
APPLICANT: Seabo, Krisatina M.
APPLICANT: Sugge, Sidney V.
APPLICANT: Sugge, Sidney V.
APPLICANT: Sugge, Sidney V.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
STREEF: 6300 Sears Tower, 233 South Wacker Drive CONNTRY: United Street Conf. Comparison of Conntry: United Street Conf. Comparison of Conntry: United Street Conntry: United Street Comparison of Conntry: United Street Conntry: United Street Comparison of Conntry: United Street Conntry: Uni
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                                                                                                       181 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNRK 203
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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MOLECULE TYPE: protein
US-09-005-243-49
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Best Local Similarity
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US-09-005-243-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                      APPLICANT: Beselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESSESE: Marshall, 0'Toole, Gerstein, Murray & Borun
STRET: 61300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COMPUTER: United States of America
ZIP: 6666-6402
COMPUTER: Edonghis FORM:
MEDIUM TYPE: Robay disk
COMPUTER: Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-AMY-1995
FILING DATE: 25-NOY-1992
FILING DATE: 32-NOY-1992
FILING DATE: 32-NOY-1992
FILING DATE: 01-6CT-1990
FILING DATE: 01-6CT-1990
FILING DATE: 01-6CT-1990
FILING DATE: 01-6CT-1990
FILING DATE: 11-UN-1990
FILING APPLICATION NUMBER: 10-UN-1990
FILING APPLICATION NUMBER: 10-U
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Sequence 48, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-005-243-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                               Gaps
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FREGERT NO. US20020031491A1

FREGEREAL INFORMATION:

APPLICANT: Bosselman, Robert A.

ADDRESSER: Grade Sears Tower, 233 South Wacker Drive

CORRESPONDENCES: 104

CONTRY: United States of America

STATE: 1111nois

COMPUTER: Table Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: BAR Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683

FILING DATE: 12-JAN-1998

FILING DATE: 12-JAN-1998

FILING DATE: 24-MAY-1995

CLASSIFICATION NUMBER: 07/982,255

FILING DATE: 25-NOV-1992

RELING DATE: 25-NOV-1992

PRIOR APPLICATION NUMBER: 07/589,701

FILING DATE: 24-MAY-1990

FRIING DATE: 24-MAY-1990
                                                                                                                                                                                                                                                               Length 273;
                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                     Score 1030; DB 3;
Pred. No. 9.2e-89;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNSK 203
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.5%;
Matches 202; Conservative
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-005-243-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-224-683-48
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                                                                                                                                                                                                                                                                                                                        121 KOLKKSFKSPEPRLFTPBEBFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                             61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                 1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                               1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Gears Tower, 233 South Wacker Drive CITY: Chicago STREET: 111inois
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELDRY ReC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CT-1990
RIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CT-1990
RIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CT-1990
RIOR APPLICATION NUMBER: 07/533,198
FILING DATE: 01-CT-1990
RIOR APPLICATION NUMBER: 07/533,198
FILING DATE: 01-CT-1990
RIOR APPLICATION NUMBER: 07/523,616
FILING DATE: 01-CT-1990
RIOR APPLICATION NUMBER: 07/523,198
FILING DATE: 11-UWN-1990
RIOR APPLICATION NUMBER: 07/523, 198
FILING DATE: 11-CT-1990
RIOR APPLICATION NUMBER: 07/523, 198
FILING DATE: 11-UWN-1990
RIOR APPLICATION NUMBER: 07/523, 198
FILING DATE: 11-UWN-1990
RIOR APPLICATION NUMBER: 07/523, 198
FILING DATE: 11-UWN-1990
RIOR APPLICATION NUMBER: 07/503, 198
   1; Indels
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/09005243
Patent No. US20020018763A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
APPLICANT: Martin, Francis H.
TILLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 01017/34465
IELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 KPFMLPPVAASSLRNDSSSSNSK 203
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/474-0448
TELEX: 25-3856
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEMYVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVBCVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILICIYLQILLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKXVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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Sequence 49, Application US/09224683

Patent No. US20020031491A1

CENERAL INFORMATION:

APPLICANT: Zeebo, Krisztina M.

APPLICANT: Suggs, Sidmey V.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS: 104

CORRESPONDENCE ADDRESS: 104

CORRESPONDENCE ADDRESS: 3030 Sears Tower, 233 South Wacker Drive CITY: Chicago

STREET: Glado Sears Tower, 233 South Wacker Drive COMPUTER: Illinois

COMPUTER: Ellinois

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: SATEM: PC-DOS/MS-DOS

SOFTWARE: PREDICATION NUMBER: US/09/224,683

FILING DATE:

COMPUTER: OFFICE TOWN DATA:

STILING DATE:

COMPUTER: OFFICE TOWN DATA:

SOFTWARE DATE OF TOWN DATA:

COMPUTER: OFFICE TOWN DATA:

SOFTWARE DATE OFFICE TOWN DATA:

COMPUTER: OFFICE TOWN DATA:

SOFTWARE DATE OFFICE TOWN DATA:

COMPUTER: O
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97.1%; Score 1030; DB 3; Length 273;
Best Local Similarity 99.5%; Pred. No. 9.2e-89;
Matches 202; Conservative 0; Mismatches 1; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1889
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRONE: 312/474-6300
TELEPRAX: 0.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KPFMLPPVAASSLRNDSSSSNSK 203
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3866

INFORMATION FOR SEQ ID NO: 48: 5 SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-09-224-683-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-224-683-49
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121 KDLKKSFKSPEPRLFTPEBFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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Patent No. US20020031491A1

GENERAL INPORMATION:
APPLICANT: Zeabo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
CORRESPONDENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Chicago
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 97.1%; Score 1030; DB 3; Length 273; Best Local Similarity 99.5%; Pred. No. 9.2e-89; Matches 202; Conservative 0; Mismatches 1; Indels (
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CLASSIFLCATION:

REGION APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,198
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/52,383
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1999
PRIOR APPLICATION NUMBER: 01/422,383
FILING DATE: 16-OCT-1999
PRIOR APPLICATION NUMBER: 01/735
FILING DATE: 16-OCT-1999
PRIOR APPLICATION NUMBER: 312/474-6300
TELEPRAM: 312/474-0418
TELECOMMUNICATION INFORMATION:
TELEPRAM: 312/474-0418
TELEFAX: 25-3856
INFORMATION PACIDS
TELEFAX: 25-3856
INFORMATION PACIDS
TELEFAX: 25-3856
INFORMATION PACIDS
TELEFAX: 313/474-0418
TELEFAX: 25-3856
INFORMATION PACIDS
TELEFAX: 313/474-0418
TELEFAX: 25-3856
TIPEL AMINO ACIDS
TELEFAX: 37-3856
TIPEL AMINO ACIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-224-683-49
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sequence 48, Application US/10175608; Publication No. US20040181044A1
GENERAL INFORMATION:
HOPLICANT: Zeebo, Krisztina M.
BOSSEGNAM, Robert A.
Suggs, Sidney V.
MATILE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                  US-10-175-608-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDLKKKSFKSPBPRLFTPEBFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/224,683
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 09/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 07/982,255
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/589,701
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATPORTY APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATPORTY AGENT INFORMATION:
NAME: CLOUGH, DAVIG M:
REGISTRATION NUMBER: 36,107
RELECOMMUNICATION NUMBER: 36,107
TELLEPRA: 3-124/74-6300
TELLEPRA: 3-124/74-6488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3866
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-224-683-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                     GITY: Chicago
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
CUNTRY: United States of America
ZIP: 6060-6402
ZIP: 6060-6402
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIPTCATION NUMBER: 09/635,249
FILING DATE: 10-AAY-1992
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/88,255
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-OW-1990
APPLICATION NUMBER: 36,107
REGERRANDNICATION INPORMATION:
REGISTRATION NUMBER: 36,107
REGERRANDNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-10-175-608-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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KPFMLPPVAASSLRNDSSSSNSK 203

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RESULT 11

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US-10-175-608-61
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                                                          CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1992
APPLICATION NUMBER: 09/486,555
APPLICATION NUMBER: 09/645,55
FILING DATE: 10-DCT-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/42,383
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 01017/35199
TELEROMUNICATION INFORMATION:
REGISTRATION NUMBER: 01017/35199
TELEROMUNICATION INFORMATION:
FELEROMUNICATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-175-608-49
Sequence 49, Application US/10175608
Sequence 49, Applicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                               181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                     KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acida
TYPE: amino acida
STRANDEDNESS: single
TOPOLOGY: linear
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1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                               61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                    1 MKKTQTWILICIYLQLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                        KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT 180
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
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     Length 273;
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STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION AUMER: 09/635,249
FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/635,249
FILING DATE: 21-DC-1993
APPLICATION NUMBER: 09/646,546
FILING DATE: 21-DC-1993
APPLICATION NUMBER: 09/646,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/593,616
FILING DATE: 10-DAR-1990
APPLICATION NUMBER: 09/593,616
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 09/573,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422,383
                                                       1; Indels
  Score 1030; DB 4;
Pred. No. 9.2e-89;
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NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
Query Match
97.1%; Score 1030; D:
Best Local Similarity 99.5%; Pred. No. 9.2e
Matches 202; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KPFMLPPVAASSLRNDSSSSNRK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                 KPFMLPPVAASSLRNDSSSSNSK 203
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Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zgebo, Krisztina M.
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Us.10-620-49
Us.10-620-642
Sequence 49, Application US/10620642
Sequence 49, Application US/10620642
Publication No. US20050080250A1
GENERAL INFORMATION:
Sugge, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
STEET: 6300 Sears Tower, 233 South Wacker Drive
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STATE: Illinois
COUNTRY: United States of America
CONTRY: United States of America
ZIP: 66060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION: <Unknown>
                                                                                                                                               AFFLICATION NUMBER: 07/502,/01

PILING DATE: 10-OCT-1991

PILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/53,198

FILING DATE: 11-JUN-1990

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 06/107/35199

TELEPHONE : 312/474-6300

TELEPHONE: 312/474-6300

TELERAX: 312/474-6300

TELERX: <UNKNOWN: 312/474-6300

TELEX: <
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US-10-620-642-48
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STRYE: Illinois STREE COUNTRY: United States of America
COUNTRY: United States of America
ZIE: 60666-6402
COMPUTER READABLE PLOPPY disk
COMPUTER READABLE PLOPPY disk
COMPUTER: 1BM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-0ct-2002
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-0ct-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,555
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 10-APR-1991
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                                                                                                                                                                                                                                                                           LENGTH: 273 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bosseiman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNRK 203
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Publication No. USZ0050080250A1
GENERAL INFORMATION:
APPLICANT: ZBEDO, Krisztina M.
                                                                                                                            TELEPHONE: 312/474-6300
                                                                                                                                                     TELEFAX: 312/474-0448
TELEX: «Untrown»
INFORWATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/175,608

PILLIA DATA 1.6 Cot-2002

APPLICATION NUMBER: 10/606

PILLIA DATA 1.6 Cot-2002

APPLICATION NUMBER: 07/406,546

PILLIA DATA 2.4 MAY-1935

APPLICATION NUMBER: 07/406,1339

PILLIA DATA 1.0 -APPLICATION NUMBER: 07/402,1339

PILLIA DATA 1.0 -APPLICATION NUMBER: 07/402,1339

PILLIA DATA 1.0 -APPLICATION NUMBER: 07/42,1331

PILLIA DATE: 1.0 -APPLICATION NUMBER: 07/42,1331

PILLIA DATE: 1.0 -APPLICATION NUMBER: 07/42,1331

PILLIA DATE: 1.0 -APPLICATION NUMBER: 07/42,1333

ATTONREY AGRETY INFORMATION:

MARIE CLOUDE, DAVIG W.

RESTERANCE OCCEST NUMBER: 01/07/3199

ATTONREY AGRETY INFORMATION:

RESTERANCE OCCEST NUMBER: 01/07/3199

ATTONREY AREA TOON NUMBER: 01/07/3199

TELECOMMUTCATION NUMBER: 01/07/3199

TELECOMUTCATION NUMBER: 01/07/31
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181 KPFMLPPVAASSLRNDSSSSNSK 203

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ALIGNMENTS

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REBULT 1

19-10-353-783-46

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19-10-351-100 No. USCO052051178A1

19-10-10-100 No. USCO052051178A1

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19-10-100 No. USCO052051178A1

19-100 No. USCO052051178A1

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US-11-176-830-508
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US-11-176-830-534
US-11-176-830-542
US-11-176-830-542
US-11-176-830-505
        App 1

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                                                                                                                                                                                                                                                                                                         US-10-620-642-46
1061
1 MKKTQTWILTCIYLQLLLEN......AASSLRNDSSSSNSKYIYLI 208
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2: /cgn2_6/ptodata/2/pubpaa/USOF NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

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Biocceleration Ltd
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US-10-353-783-48
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US-10-353-783-51
US-10-353-783-52
US-11-176-830-520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117670 segs, 14887254 residues
                                version -
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                GenCore (c) 1993
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyright
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Match
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Perfect score:
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6006-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
PILING DATE: 24-AUG-1990

APPLICATION NUMBER: 07/537,198

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989

ATTORREY/AGENT INPORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER:

TELEFORMUNICATION INFORMATION:

TELEFORM: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 97.1%; Score 1030; DB 6; Best Local Similarity 99.5%; Pred. No. 7.5e-86; Matches 202; Conservative 0; Mismatches 1;
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FILING DATE: 28-Jan-2003
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATE:
APPLICATION DATE:
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bosselman, Robert A. Suggs, Sidney V. Martin, Francis H. TITLE OF INVENTION: Stem Cell Factor NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
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Publication No. USZ0050261175A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-10-353-783-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KDLKKSFKSPEPRLFTPBEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                          Length 208;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1061; DB 6; Best Local Similarity 100.0%; Pred. No. 8.5e-89; Matches 208; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-3an-2003
CLIASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 46: US-10-353-783-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/573,616
                           TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERIZFICS:
LENGTH: 208 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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US-10-353-783-48
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Gaps

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Length 273;

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-5an-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin, Francia H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-353-783-61
      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KPFMLPPVAASSLRNDSSSSNRK 203
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; Publication No. US20050261175A1
; GENERAL INFORMATION: Krisztina M.
; APPLICANT: Zsebo, Krisztina M.
; Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 273 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.5<sup>3</sup>
Matches 202, Conservative
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US-10-353-783-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STRET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/10353783;
Publication No. US20050261175A1
GENERAL INFORMATION: Tasebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
               FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 22-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-ON-1990
APPLICATION DATE: 11-ON-1990
APPLICATION DATE: 11-ON-1990
APPLICATION DATE: 11-ON-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-353-783-49
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TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-353-783-61
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MDVLPSHCMISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-APR-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/52,383
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/522,383
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-DW-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-OW-1990
APPLICATION NUMBER: 01017/32958A
TELECOMMUNICATION NUMBER: 01017/32958A
TELECOMMUNICATION NUMBER: 01017/32958A
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99.5%; Pred. No. 7.5e-86;
tive 0; Mismatches 1;
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US-10-353-783-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                               STATE: Illinois
COUNTX: United States of America
CUNTX: United States of America
ZIP: 60606-6402
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-0DS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: CUNKNOWn>
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APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
APPLICATION NUMBER: 08/172,329
APPLICATION NUMBER: 07/692,255
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/694,535
FILING DATE: 02-MPR-1992
APPLICATION NUMBER: 07/699,101
APPLICATION NUMBER: 07/699,101
APPLICATION NUMBER: 07/699,101
APPLICATION NUMBER: 07/63,616
FILING DATE: 01-0CT-1990
APPLICATION NUMBER: 07/631,198
FILING DATE: 16-0CT-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1999
ATTORINY/AGENT INPORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
STRANDEDNESS: single
SEQUENCE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-353-783-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 KPFMLPPVAASSLRNDSSSSNRK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 273 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                             Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Clough, David W. REGISTRATION UNDRER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
APPLICATION NUMBER: 07/684,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589, 701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573, 616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537, 198
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/422, 383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
Sequence 57, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 266 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS
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Best Local Similarity 92.6
Matches 188; Conservative
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us-10-620-642-46.rapbn

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Sequence 520, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gartienti, Lila

APPLICANT: Gartienti, Lila

APPLICANT: OFITCHANTION: Rational Evolution of Cytokines for Higher Stability, Encoding Ni

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 17109-012002 (922B)

CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT APPLICATION NUMBER: 10/658,834

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR PILING DATE: 2003-09-08

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSFKSPEPRLFTPEEFFRIFN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDIKKSFKSPERFTFTPEEFFRIFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAASSLRNDSSSSNRK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 RSIDAFKOFVVASETSDCVVSSTLSPEKOSRVSVTKPFMLPPVAASSLRNDSSSSNSK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 EGICRNRVTINNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
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                                                                                                                                                                                                                                                                                                                                                                         Query Match

84.6%; Score 898; DB 7; Length 248;
Best Local Similarity 99.4%; Pred. No. 5.3e-74;
Matches 177; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                ) ORGANISM: Homo sapiens

) PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Genbank AAA85450

); DATABASE ENTRY DATE: 1996-01-19

US-11-176-830-206
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 520
LENGTH: 248
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Matches 176, Conservative
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US-11-176-830-520
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                                                                                                                                                                     APPLICANT: CHUNG, Yong-Hoon
APPLICANT: LEE, Hak-sup
APPLICANT: LEE, Hak-sup
APPLICANT: KIM, Jae-Youn
APPLICANT: KIM, Jae-Youn
APPLICANT: KIM, Jae-Youn
APPLICANT: KIM, Jae-Youn
APPLICANT: HEO, Youn-Head of improving efficacy of biological response-modifying
TITLE OF INVENTION: proteins and the example muteins
TITLE OF INVENTION: Droteins and the example muteins
TITLE OF INVENTION WIMBER: US/10/519,390
CURRENT APPLICATION NUMBER: KR10-203
PRIOR PLICATION DATE: 2003-07-26
NUMBER OF SEQ ID NOS: 65
SEQ ID NOS: 65
SEQ ID NO 24
LENGTH: 248
TYPE: NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2006, Application US/11176830

| Sequence 2006, Application US/11176830
| Publication No. US2006002016A1
| GENERAL INFORMATION:
| APPLICANT: Ganier, Rene
| APPLICANT: Usea, Manuel
| APPLICANT: Usea, Manuel
| TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NurITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NurITLE OF INVENTION: Rational Evolution of Cytokines
| TITLE OF INVENTION: Rational Evolution of Cytokines
| FILE REPRENENCE: 17109-01202 (922B)
| CURRENT FILING DATE: 2003-09-08
| PRIOR PILING DATE: 2003-09-08
| PRIOR PILING DATE: 2003-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: SCP: 63rd, 102nd, 110th, 115th, 116th, 119th, 126th, 129th, ; OTHER INFORMATION: 158th, 199th, 205th, 207th or 245th Phe is replaced by Val. US-10-519-390-24
   121 KOLKKSFKSPEPRLFTPEBFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                    96 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
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                                                                                                                                                   181 KPFMLPPVAASSLRNDSSSSNSK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 529, Application US/11176830

Sequence 529, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Rene

APPLICANT: Drittanti, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Manuel

ITILE OP INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nn.

TITLE OP INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nn.

TITLE OP INVENTION: Acid Molecules and Related Applications

TITLE OP INVENTION: Acid Molecules and Related Applications

CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT PILING DATE: 2005-07-06

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR APPLICATION NUMBER: 5002-09-09

NUMBER: OF SEQ ID NOS: 1306

SEQ ID NO 529

LENGTH: 248

PRIOR PRIOR APPLICATION NUMBER: 60/409,898

PRIOR PRIOR APPLICATION NUMBER: 50/409,898

PRIOR PRIOR APPLICATION NUMBER: 50/409,898
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                                                Length 248;
                                           Query Match

84.4%; Score 895; DB 7;

Best Local Similarity 98.9%; Pred. No. 9.9e-74;

Matches 176; Conservative 1; Mismatches 1;
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Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: GayOu, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-11-176-830-529
US-11-176-830-519
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                                                                                   Sequence 537, Application US/11176830

| Sequence 537, Application US/11176830
| Publication No. US20060020116Al
| GENERAL INFORMATION:
| APPLICANT: Gantier: Rene
| APPLICANT: Guyon, Thierry
| APPLICANT: Drittanti, Lila
| APPLICANT: Dritanti, Lila
| APPLICANT: Now Ranical
| TITLE OF INVENTION: Acid Molecules and Related Applications
| FILE REPRENCE: 11709-012002 (922B)
| CURRENT APPLICATION NUMBER: US/11/176,830
| CURRENT APPLICATION NUMBER: 60/457,135
| PRIOR FILING DATE: 2003-09-08
| PRIOR FILING DATE: 2003-09-09
| RINGR APPLICATION NUMBER: 60/409,898
| PRIOR FILING DATE: 2003-09-09
| NUMBER OF SEQ ID NOS: 1306
| SEQ ID NO 537
| LENGTH: 248
| LENGTH: 248
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; ORGANISM: Homo sapiens
US-11-176-830-537
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US-11-176-830-519
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Sequence 499, Application US/11176830

Sequence 499, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gardier, Rene
APPLICANT: Gardier, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Arational Evolution of Cytokines for Higher Stability, Encoding Ni TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (922B)
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (922B)
FILE REFERENCE: 1709-012002 (922B)
FILE REFERENCE: 1700-012002 (922B)
FILE REFERENCE: 2003-09-08
FILE REFERENCE: 2003-09-09
FILE REFERENCE: 2002-09-09
FILE REFERENCE: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
FILE REFERENCE: 1306
FILE REFERENC
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            61 DKFSNISBGLSNYSIIDXLVNIVDDLVBCVKRNSSKDLKKSFKSPEPRLFTFEBFFRIFN 120
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84.3%; Score 894; DB 7;

Best Local Similarity 98.9%; Pred. No. 1.2e-73;

Matches 176; Conservative 1; Mismatches 1;
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Job time : 9.02204 secs
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CORGANISM: Homo sapiens
US-11-176-830-499
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US-11-176-830-499
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TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REPRENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR PRILING DATE: 2005-07-08
PRIOR PLING DATE: 2003-09-08
PRIOR PLING DATE: 2003-09-09
PRIOR PLING DATE: 2003-09-09
PRIOR PLING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SEQ ID NOS: 1306
SEQ ID NO 5:36
LENGTH: 248
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US-11-176-830-536
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US-11-176-830-538
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US-11-176-830-538
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Title: Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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New naturally-occurring polypeptide stem cell factor analogues haematopoietic biological activity of stem cell factor and are treat e.g. leukopenia, AIDS, nerve damage and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Stem cell factor; SCF; leukopenia; AIDS; haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human Stem Cell Factor from HT1080 fibrosarcoma line
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                                                                                                                                                                                                                                                                                    ALIGNMENTS
ADW93106
ADZ4758
ADZ4758
AAB98366
AAU02458
AAU02765
AAU02766
AAU0276648
ADS99318
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AAR32166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .25
/label= sig_peptide
26. .273
/label= mat-protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               AAR11711 standard; protein; 273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-00422383.
90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
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 Zsebo KM, Suggs SV,
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N-PSDB; AAQ11542.
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11-JUN-1990;
24-AUG-1990;
28-SEP-1990;
01-OCT-1990;
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Peptide
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 Pebruary 22, 2006, 18:05:41 ; Search time 160.566 Seconds
(without alignments)
747.047 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                               US-10-620-642-61
1397
1 MKKTQTWILTCIYLQLLLFN......NBEDNRISMLQBKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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Aar83978
Aar83978
Aar83564
Aar98357
Aar98357
Aar98692
Aar98692
Aar98692
Aar98692
Aar98692
Aar986932
Aar98642
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Aar989331
Aar989331
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Biocceleration Ltd.
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                                                                                                                                                                                                                       2443163 segs, 439378781 residues
           GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           protein search, using sw model
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AAR33978
AAR33978
AAX53284
AAB98357
AAU02460
AAB96942
AAB96942
AAB96942
AAB96942
AAB96942
AAB96942
AAB96942
AAB96943
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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4.0.07.99

Result

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The SCF has the ability to stimulate growth of primitive progenitors including early hematopoietic progenitor cells and non- hematopoietic

Disclosure; Fig 42; 127pp; English

Human Human Human Human Human

ADP99319 ADUS0661 ADUS0649 ADW93094

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(first entry)
                                                                                                                                                                                                Sest Local Similarity 100.
                Lyman S;
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                              WPI; 1992-041558/05.
                                      N-PSDB; AAQ20845.
                                                                                                                                                                            Sequence 273 AA;
                Williams DE,
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15-MAY-1996
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       germ stem cells. The
stem cells such as neural stem cells and primordial germ stem cells. The product may be used in a pharmaceutical compsn. for treating, in a mammal, leukopenia, thrombocytopenia, anaemia, AIDS, neoplasia, nerve damage, infertility and intestinal damage. See also AAR11708, AAQ11509-011543
                                                                                                 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKCR
                                                                                                                                                                                          KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                    Gaps
                                                                                   ·;
                                                                    Length 273;
                                                                                                                                                                                                                                                                                                                                              hMGF-2.4; hematopoietin; interleukin; IL-3; c-kit oncogene; proliferation.
                                                                             133;
0; Indels
                                                                   100.0%; Score 1397; DB 2;
100.0%; Pred. No. 2.2e-133;
iive 0; Mismatches 0;
                                                                                                                                                                                                                       OPSLIRAVENIQINEEDNEISMLQEKEREFQEV 273
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                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .25
/label= signal
26 . .210
/label= extracellular
/note= "claimed polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= transmembrane
238. .273
/label= intracellular
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90US-00565840.
90US-00574152.
90US-00586073.
                                                                                                                                                                                                                                                                                                                                Human mast cell growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-00543264
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 .237
                                                                         Best Local Similarity 100.
Matches 273; Conservative
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30-APR-1992 (first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
                                                     Sequence 273 AA;
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28-AUG-1990;
21-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                    Query Match
Best Local S
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This human MGF has a mature extracellular region of 185 amino acids. There is a second form of hMGF (see AAQ20844) resulting from an additional use mind splicing event which deletes an exon encoding an additional 28 amino acids beginning at amino acid 148 of the mature protein. MGF is the ligand for the protein receptor expression product of the c-kit proto-oncogene. MGF can be used to augment the activity of other cytokines. It can influence early lymphoid or myeloid development. See also AAQ20842-3 and AAQ22204-7. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                               to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated DNA encoding human mast cell growth factor - useful in stimulating proliferation of haematopoietic cells with growth factor, treat haemolytic and hypo;proliferative anaemias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKOVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stem cell factor; progenitor; haematopoiesis; SCF; anaemia; thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft; transplant; neoplasia; myelosuppression; bone marrow; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human stem cell factor derived from HT1080 fibrosarcoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1397; DB 2; Length 273; 100.0%; Pred. No. 2.2e-133; ive 0; Mismatches 0; Indels 0;
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    /label= sig_peptide
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    /label= mat_SCF

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                                                                                                                     Claim 10; Fig 4; 59pp; English
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This sequence represents a membrane bound form of a human recombinant stem cell factor (SCF). Stem cell factors are also known as mast cell growth factors (MCF). Stem cell factors (SF or SLF) are haematopoietic type SCF sequence (MCF) or Steel factors (SF or SLF) are haematopoietic factors which act on haematopoietic progenitor cells. Analogues of a wild type SCF sequence have been constructed (see AAW27605 and AAW27606) which have increased blological activity and stability compared to unmodified SCF and can be used treat pigmentation disorders, e.g. vitilago, acquired immunodeficiency syndrome, nerve damage, infertility, intestinal damage canaemia, enhance bone marrow engraftement during transplantation or bone marrow recovery following radiation, chemical or chemotherapeutic, induced bone marrow aplasia or myelosuppression, sensitise cells to chemotherapy or mobilise peripheral blood progenitor cell, preferably bone marrow or peripheral blood progenitor cell, preferably bone marrow or peripheral blood progenitor cell, uniture medium, where the cells are optionally subsequently transfected with exogenous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stem cell factor analogue N10D or N10D/N11D - useful to treat pigmentation disorder, AIDS, nerve damage, infertility, intestinal damage or haematopoietic disorder.
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                                                                                                  Stem cell factor; SCF; mast cell growth factor; MCGF; Steel factor; SF; SLF; analogue; treatment; haematopoietic factor; progenitor cell; pigmentation disorder; haematopoietic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKKTQTWILICIYLQLLLENPLVKTEGICRNRVTNNVKOVTKLVANLPKOYMILKYVPG
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                                                                                                                                                                                                                                                                    1. .25
/label= leader sequence
/label= leader sequence
/note= "mature full length stem cell factor protein"
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                                                               Human recombinant stem cell factor protein.
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR83978 is a human stem cell factor (SCF) derived from the HT1080
fibrosarcoma cell line. Non-naturally occuring SCF and C-terminally
cruncated polypetides, having amino acid sequences sufficiently
duplicative of naturally occurring SCF, stimulate growth of printive
progenitors such as haematopoietic progenitor cells, neural stem cells
and primordial germ stem cells. The peptides can be used in a composition
for treating leucopenia, anaemia or thrombocytopenia, for enhancing
engraftment of bone marrow during transplantation or for bone marrow
convery after chemotherapy or radiation-induced bone marrow application or myelosuppression. They can also be used for treating neoplasia, nerve
damage, infertility, intestinal damage or myeloproliferative disorders.
Antibodies may be raised against the peptides for use in detection or
cutralisation of SCF in serum. SCF may be useful for the treatment of
AIDS and severe combined immunodeficiency (SCID) states alone or in
combination with other factors such as IL-7. (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOLKKSPKSPERLFTPEEFFRIFNRSIDAPKOPVVASETSDCVVSSTLSPEKDSRVSVT
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                                                                                                                                                                                                                                                                                           Martin FH;
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                                                                                                       89US-00422383.
90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
                                                                 95EP-00105391
                                                                                                                                                                                                                                                                                           Zsebo KM, Suggs SV,
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                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 273 AA;
                                                               04-OCT-1990;
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Claim

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181 181 241 AAW27607

AAW27607 RESULT

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WPI; 2001-366062/38.
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                                       Similarity
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    Sequence 273 AA;
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21-DEC-1993;
24-MAY-1995;
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01-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                Administration to a subject. The method comprises: (a) obtaining haematopoietic progenitor cells from a donor; and (b) expanding the cells haematopoietically effective dose of a by adding to the cells a haematopoietically effective dose of a confirmation and one or more of the brimary structural properties of naturally confirmation and one or more of the biological properties of naturally cocurring stem cells factor (SCP). The method is useful for stimulating primitive progenitor cells including early haematopoietic progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, granulocyte, lymphocyte and macrophage cells. SCP results in absolute increases in haematopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic progenitors in syngeneic, allogeneic for expanding early haematopoietic progenitors in syngeneic, allogeneic cells. SCP is useful for treating haematopoietic progenitors in syngeneic, allogeneic cells. SCP is useful for renaplant. SCF is useful for enhancing the cefficiency of gene therapy based on transfecting haematopoietic seconds. Cells. SCP is also useful for combacting the myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing haematopoietic recovery cellering cancer acute blood loss and as a boost to the immune system for fighting compassa (claimed human SCF from the present invention
Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
                                                                                                                                                                                                                                      forming;
                                                                                                                                                                                                                                    Stem cell factor; SCF; haematopoietic progenitor cell; blood forming primitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; autologous bone marrow transplant; gene therapy; transfection; heematopoietic stem cell; acute blood loss; neoplasia;
                                                                                                                                                                                                           Human SCF protein isolated from the HT1080 fibrosarcoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martin FH;
                                                     241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                        OPSLIRAVENIQINEEDNEISMLQEKEREFQEV 273
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                                                                                                                                 AAY53284 standard; protein; 273
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90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
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N-PSDB; AAA13714.
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04-OCT-1990;
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                                                                                                                          1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKOYMITLKYVPG
                                                                                                                                                                                                                    61 MDVLPSHCWISEMVVQLSDSLTDLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                               1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                             KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                    Gaps
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Length 273;
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100.0%; Score 1397; DB 3;
100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human SCF protein sequence SEQ ID NO:61
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90US-00537198.
90US-00573616.
90US-00589701.
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93US-00172329.
95US-00449653.
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                                                    Matches 273; Conservative
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vitro, comprising exposing (II) that expresses a stem cell factor (SCF) receptor to a biologically active SCF, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a useful in gene therapy techniques. Addition to Addition of the present equences used in the exemplification of the present
                                                                                                                                                                                                                                                                 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                            9
                                                                                                                                                                                                               factor; SCF; stem cell factor receptor; blood cell disorder;
                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLPNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                  121 KOLKKSFKSPEPRLFTPEEFFRIFURSIDAFKDFVVASETSDCVVSSTLSPEKOSRVSVT
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                                                                                                                                                 Query Match 100.0%; Score 1397; DB 4; Length 273; Best Local Similarity 100.0%; Pred. No. 2.2e-133; Matches 273; Conservative 0; Mismatches 0; Indels 0
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90US-00537198.
90US-00573616.
90US-0059701.
92US-00982255.
93US-00172329.
95US-00449653.
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                                                                                                                           Sequence 273 AA;
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therapy.
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11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
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12-JAN-1998;
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                                                                                                                               The present invention describes a method for enhancing (B) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCP) receptor to a biologically active SCP, its analogue of fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a atarget mammalian efficiency of the transfer of a useful in gene therapy techniques. AAM41301 to AAM41364 and AAB98351 to AAB98390 represent sequences used in the exemplification of the present
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                                         Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide into cell in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                             KOLKKSPKSPEPRLFTPEEFPRIFNRSIDAPKOFVVASETSOCVVSSTLSPEKOSRVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; stem cell factor; SCF; early haematopoietic progenitor cell;
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                                                                                                                                                                                                                                                                                                                       Length 273;
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100.0%; Score 1397; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.2e-133;
Matches 273; Conservative 0; Mismatches 0;
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/label= Signal_peptide
26. .273
/label= Mature_SCF
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                                                                                                         Example 3; Fig 16; 210pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaemia; Kala azar;
HT1080 fibrosarcoma.
                                                                                                                                                                                                                                                                                              Sequence 273 AA;
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                                                                                                                                                                                                                                                                      invention
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Protein
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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFs). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukacemias, haematopoietic disorders, aplastic anaemia, paroxysmal naemoglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is an SCF described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            stimulating growth of early hematopoietic progenitor cells, useful fo
treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
                                                      Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                               cell factor polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                    Martin FH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated non-human mammalian stem
                              Human stem cell factor SEQ ID NO: 49.
                                                                                                                                                                                                                                                                                                                                                                                    Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 16; 209pp; English.
                                                                                                                                                                                                                                                           89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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13-JUL-2001 (first entry)
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Matches 273; Conservative
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                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 273 AA;
                                                                                                                                       Homo sapiens.
                                                                                                                                                                   US6207802-B1
                                                                                                                                                                                                                               09-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sarcoidosis.
                                                                                                                                                                                                                                                                                           24-AUG-1990;
01-OCT-1990;
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                                                                                                                                                                                                                                                                           Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMILKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%; Score 1397; DB 4; Length 273; Local Similarity 100.0%; Pred. No. 2.2e-133; nes 273; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                    Suggs SV, Martin FH;
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                                           90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
95US-00482918
                               89US-00422383
                                                                                                                                                                                                    Zsebo KM, Bosselman RA,
                                                                                                                                      BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                 2001-298941/31.
                                                                                                                                                                      MARTIN F H.
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                                                                                                                         ZSEB/) ZSEBO
                                              11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
                                                                                           21-DEC-1993;
   07-JUN-1995;
                               16-0CT-1989
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Query Match

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Gaps

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Length 273; Indels 180

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AAB96942

AAB96942

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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, sarcoidosis.
KDLKKSPKSPEPRLPTPEBPPRI PNRSI DAPKD FVVASETSDCVVSSTLSPEKDSRVSVT
               121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAPKOFVVASETSOCVVSSTLSPEKDSRVSVT
                                                 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALPSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                     Human, rat, mammal, stem cell factor, SCF, cell growth stimulation, gene therapy, haematopoietic disorder, aplastic anaemia, leukaemia, neurological damage, intestinal damage, infertility, AIDS, SCID,
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/label= signal_peptide
26. .273
/label= mature_stem_cell_factor
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                                                                                                  Suggs SV, Martin
                                                                                                                                                                                                                                                                            Human stem cell factor SEQ ID NO: 61.
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                                                                                                                                                                                                                                                                                                                                               severe combined immunodeficiency.
                                                                                                                                                                                               AAB96952 standard; protein; 273
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90US-00537198.
90US-00573616.
90US-00589701.
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hemacopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, sarcoidosis
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                                                                                                                            Human; rat; mammal; stem cell factor; SCP; cell growth stimulation; gene therapy; haematopoletic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
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                                                                                                                                                                                                                                                                           /label= mature_stem_cell_factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin FH;
                                                                                                                                                                                                                                    1. .25
/label= signal_peptide
                                                                                                   stem cell factor SEQ ID NO: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 15D; 209pp; English.
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                       AAB96941 standard; protein; 273
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90US-00537198.
90US-00573616.
90US-00589701.
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                                                                            entry)
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N-PSDB; AAF89102.
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01-OCT-1990;
25-NOV-1992;
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11-JUN-1990;
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                                                AAB96941;
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The present sequence representing human SCF (stem cell factor) protein is isolated from the HT1080 fibrosarcoma cell line. The present invention cals isolated from the HT1080 fibrosarcoma cell line. The present invention cells to perform cell factors (AAB73561-AAB73557) and the polymucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also central peptides (AAB7378-AAB73579) and the oligonucleotides (AAB73895) used in the isolation of human and rat SCF sequences. (AAB723895-AAB73895) used in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in CC gene therapy. It is useful for treating disorders involving blood cells cauch as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hoddkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicaemia, malaria, vitamin Blz and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOLKKSFKSPERPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 MDVLPSHCWISEWVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                    Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1397; DB 4;
100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
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/label= Signal peptide
Claim 7; Fig 42A-42C; 166pp; English.
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/label= Mature_SCF
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                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                  Sequence 273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6218148-B1
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                          MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                      KDLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
                                                                                                                    1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMILKYVPG
                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                            KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                                                                                                                                                                KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                    MKKTQTW1LTC1YLQLLLFNPLVKTEG1CRNRVTNNVKDVTKLVANLPKDYM1TLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, stem cell factor, SCF, early haematopoietic progenitor cell;
blood disorder, leukaemia; Hodgkin's disease, lymphoma; splenomegaly;
anaemia; Kala azar, septicaemia, malaria; hypopigmentation disorder;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human SCF protein isolated from the HT1080 fibrosarcoma cell line
                                                          ö
                    Length 273;
                                                        0; Indels
                  100.0%; Score 1397; DB 4;
100.0%; Pred. No. 2.2e-133
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                          OPSLIRAVENIQINEEDNRISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                    241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l. .25
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB73567 standard; protein; 273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26. .273
/label= Mature_SCF
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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                                                          Matches 273; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-256683/26.
N-PSDB; AAH23901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HT1080 fibrosarcoma
                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6204363-B1
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240

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Gaps

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120

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The present sequence represents human stem cell factor (SCF). The cDNA encoding this sequence is isolated from the HT1080 fibrosarcoma cell line. The sequence is described in an invention relating to novel stem cell factors, the polynucleotides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor cells in human peripheral blood by administering a haematopoietically effective human stem cell factor including myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, ilymphoma, qaucher's disease, Niemann-Pick disease, refractory anaemia, milataia, vitamin B12 and folic acid deficiency, hypopigmentation disorders i.e. piebaldism and viral induced disorders, including AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
Human, stem cell factor; SCF; haematopoietic progenitor cell; AIDS; blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency; hypopigmentation disorder; viral disorder; HT1080 fibrosarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKTQTW1LTC1YLQLLLFNPLVKTEG1CRNRVTNNVKDVTKLVANLPKDYM1TLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1397; DB 4;
100.0%; Pred. No. 2.2e-133;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suggs SV, Martin FH;
                                                                                                                                                                                                                                                           'note= "Encoded by ATT"
                                                                                                                                                    1. .25
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                    /note= "Encoded by ATT'
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                           26. .273
/label= Mature_SCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 42; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900S-00573616.
900S-00589701.
910S-00684535.
92US-00982255.
93US-00172329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZSEBO K M.
BOSSELMAN R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-407312/43.
                                                                                                                                                                                                                                                                            Misc-difference 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BOSS/) BOSSBLMAN R
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-AUG-1990;
01-OCT-1990;
10-APR-1991;
25-NOV-1992;
21-DEC-1993;
                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                              US6248319-B1
                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2001
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                                                                                                                                                    Protein
                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                The present sequence representing human SCF (stem cell factor) protein is isolated from the HT1080 fibrosarcoma cell line. The present invention relates to novel stem cell factors (AAU02776, AAU02770-AAU02775, AAU02797) and the polymuclectides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the olymuclectides (AAU02777-AAU02794) and the cincention also describes SCF peptides (AAU02777-AAU02794) and the cat SCF sequences. The polymuclectide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating producing SCF and useful in gene therapy. It is useful for carcinoma, acute leukaemia, multiple myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myelofibrosis, military tuberculosis, disseminated fungus disease, lancomegaly, military tuberculosis, disseminated fungus disease, bulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDXLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPFML.PPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                  , encoding polypeptide product useful for early hematopoietic progenitor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1397; DB 4; Length 273; 100.0%; Pred. No. 2.2e-133; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                              Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPSLIRAVENIQINEEDNEISMLOEKEREFOEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 OPSLTRAVENIOINEEDNEISMLOEKEREFOEV 273
                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 42A-42C; 167pp; English.
                                                                                                                                                                                           Sugga SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
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                        89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
                                                                                                           92US-00982255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 273; Conservative
                                                                                                                                                                                              Bosselman RA,
                                                                                                                                                                                                                                                                                                  Isolated DNA sequence, stimulating growth of e
                                                                                                                                                                                                                                   WPI; 2001-281051/29.
N-PSDB; AAS04224.
                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and vitiligo
                                                                                                           25-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2001
                                                                                       01-OCT-1990
                          16-OCT-1989
                                             .1-JUN-1990
                                                                 24-AUG-1990
                                                                                                                                                                                              Zaebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
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                KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                     KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                        KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel non-naturally-occurring stem cell factor polypeptide, useful treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Mature human SCF protein"
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/label= Signal_peptide
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(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                      Human SCF protein #2.
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N-PSDB; AAD35477
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Search Job time

The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally-occurring SCF to allow possession of haematopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia,

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consemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemorkerapeutic induced bone marrow aplasia or myclosuppression. They care also useful for treating acquired immune deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal camage, neoplasia, infertility, myeloproliferative disorder, intestinal camamal. STG sequences are useful for preparing blologically active polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing transfection of early cative polymer polypeptide adduct, for enhancing transfection of early categopetrosis, metastatic carcinoma, acute leukaemia, myeloslarosis, osteopetrosis, metastatic carcinoma, acute leukaemia, myeloma, costeopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hoddkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Siwe disease, refractory erythroblastic anaemia, pi Guglielmo sylandrome, congestive splenomegaly, Kala azar, asarcoidosis, primary splenomegaly, mand azar, asarcoidosis, primary caplenic pancycopaemia, diseaminated fungue disease, malaria, military tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin B12 and folic acid deficiency, plamond Blackfan anaemia, hypopigmentation disorders such as piebaldism, AIDS (acquired immune deficiency syndrome) conductiligo. The present sequence is human SCF protein
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Best Local Similarity 100.
Matches 273; Conservative
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Biocceleration Ltd.
 GenCore version
Copyright (c) 1993 - 2006
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OM protein - protein search, using sw model

Run on:

Pebruary 22, 2006, 18:13:23 ; Search time 22.562 Seconds
(without alignments)
1164.223 Million cell updates/sec

US-10-620-642-61 1397 1 MKKTQTWILTCIYLQLLLFN......NBEDNEISMLQEKEREPQEV 273 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	mast cell growth f	mast cell growth f	c-kit ligand - pig	facto	stem cell factor -	mast cell growth f	Н	stem cell factor p	_	stem cell factor p	stem cell factor 1	stem cell factor s	stem cell factor -	cell			hypothetical prote	probable advanced	conserved hypothet	probable membrane	hypothetical prote	hypothetical prote		hypothetical prote		cell-division init	hypothetical prote	paired box transcr	F
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ALIGNMENTS

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RESULT 1 A35974	S	N;Alternate names: kit ligand; stem cell factor	ect	te:	C; Accession: A35974; A61190	rti	ပ	63	tle	A; Reference number: A35974; MUID: 91004219; PMID: 2208279	A; Accession: A35974	A. Mologisto tropo month
RESULT A35974	nast	1;A1	;; Sp	, Da	.; Ac	, Ma	٦,	e11	\;Ti	1; Re	1; AC	7
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9-Jul-2004

kino, K.H.; Morris, C.F Wypych, J.; Sachdev, F uman stem cell factor [A; Molecule type: mRNA A; Residues: 1-273 skNAs. A; CrossareEernces: UNIPROT: P21583; UNIPARC: UPI000002D482; GB: M59964; NID: 9337933; PIDN B; Anderson, D.M.; Williams, D.B.; Tushinski, R.; Gimpel, S.; Eisenman, J.; Cannizzaro, J. Cell Growth Differ. 2, 373-378, 1991 A; Title: Alternate splicing of mRNAs encoding human mast cell growth factor and localiza A; Reference number: A61190; MUID: 92172791; PMID: 1724381

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-273 <AND>
A;Residues: 1-273 <AND>
A;Cross-references: UNIPARC:UPI00002D482 C, Genetics:

A;Gene: GDB:MGF
A;Cross-references: GDB:128026; OMIM:184745
A;Cross-references: GDB:128026; OMIM:184745
A;Cross-references: GDB:128021422
C;Superfamily: mouse mast cell growth factor
C;Superfamily: mouse mast cell growth factor
C;Keywords: alternative splicing; extracellular protein; glycoprotein; transmembrane prc
F;1-25/Domain: signal sequence #status predicted <8GS
F;2-273/Product: mast cell growth factor; soluble form #status predicted <1
F;26-139/Product: (or 26-190) most cell growth factor, soluble form #status predicted <1
F;26-237/Domain: transmembrane #status predicted <TWM>
F;215-237/Domain: transmembrane #status predicted <TWM>

ô Gaps ö Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 2e-101; Matches 273; Conservative 0; Mismatches 0; Indels 0

61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 g g Š ò

121 KOLKKSFKSPEPRLFTPEBFFRIFNRSIDAFKDFVVASFTSDCVVSSTLSPBKDSRVSVT 180

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-274 <ZHA>
A;Residues: 1-274 <ZHA>
A;Cross-references: UNIPROT: Q29030; UNIPARC: UPI0000135640; GB:L07786; NID:g164420; PIDN: C;Superfamily: mouse mast cell growth factor
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Superfamily: mouse mast cell growth factor
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84.8%; Score 1184.5; DB 2; Length
Best Local Similarity 84.7%; Pred. No. 7.1e-85;
Matches 232; Conservative 20; Mismatches 21; Indels
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86.1%; Score 1203.3; July
Best Local Similarity 85.8%; Pred. No. 2.4e-86;
Matches 235; Conservative 22; Mismatches 16;
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146575
G-kit ligand - pig
C.Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146575
B;Zhang, Z.; Anthony, R.V.
Biol. Reprod. 50, 95-102, 1994
A;Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization A;Reference number: 146575; MUID:94146218; PMID:7508758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212
                                                      MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                      QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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A; Molecule type: mRNA
A; Residues: 1-206,'S',208-270 <HUZ>
A; Cross-references: UNIPARC:UPI000017955D; GB:M38511
R; Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Bisenman, J.; Rauch, C.; March, Cell 63, 235-243, 1990
A; Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in A; Reference number: A35977; MUID:91004223; PMID:169858
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Moeldudes: 1-273 - AND.
A; Cross-references: UNIPARC: UP10000028C9B; GB: MS7647; GB: M38436; NID: 9199151; PIDN: AAA3-
R; Copeland, N.G.; Gilbert, D.J.; Cho, B.C.; Donovan, P.J.; Jenkins, N.A.; Cosman, D.; Acell 63, 175-183, 1990
Cell 63, 175-183, 1990
A; Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and i
A; Reference number: A35972; MUID: 91004216; PMID: 1698554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 26-33 <COP>
A;Cross-references: UNIPARC:UPI000017955B; GB:M59912
A;Cross-references: UNIPARC:UPI000017955B; GB:M59912
B;Zsebo, K.M.; Williams, D.A.; Geissler, B.N.; Broudy, V.C.; Martin, P.H.; Atkins, H.L.,
Cattanach, B.M.; Galli, S.J.; Suggs, S.V.
A;Title: Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for A;Reference number: A35975; MUID:91004220; PMID:1698556
A;Accession: A35975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-201 2.525.
A; Residues: 1-201 2.525.
A; Cross-references: UNIPARC: UPI000016D02D; GB: M59915; NID: g200935; PIDN: AAA40095.1; PID
R; Zsebo, K.M.; Mypych, J.; McNiece, I.K.; Lu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev,
R; Langlay, K.B.
Cell 63, 195-201, 1990
A; Title: Identification, purification, and biological characterization of hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP1000017955F
R;Brannan, C.I.; Bedell, M.A.; Resnick, J.L.; Eppig, J.J.; Handel, M.A.; Williams, D.E.,
Genes Dev. 6, 1832-1842, 1992
A;Title: Developmental abnormalities in Steell?H mice result from a splicing defect in t
A;Reference number: A44071; MUID:93012940; PMID:1383087
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A;Molecule type: mRNA
A;Residues: 1-206,'S',208-273 <RES>
A;Cross_references: UNIPARC:UPIO00016CA07; EMBL:X68989; NID:g395283; PIDN:CAA48778.1; PI
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C;Keywords: extracellular protein; glycoprotein, transmembrane protein
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82.8%; Pred. No. 9.8e-83;
ive 19; Mismatches 28;
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A;Molecule type: protein
A;Residues: 27-29,'R',31-39 <ZS2>
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Matches 226; Conservative
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S65801
mast cell growth factor - mouse
NyAlternate names hematopoietic growth factor KL; ligand steel factor; stem cell factor
C;Species Mus musculus (house mouse)
C;Date: 28 - Oct-1996 #sequence revision 27-Feb-1997 #text change 09-Jul-2004
C;Date: 28 - Oct-1996 #sequence revision 27-Feb-1997 #text change 09-Jul-2004
C;Accession: S65801; A43751; Ā35976; A35977; A35975; A35975; A35973; I48768
R;Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 327-934, 1996
A;Title: Multiple pathways for Steel regulation suggested by genomic and sequence analys
A;Reference number: S65801; MUDD:97002551; PMID:8849898
A;Accession: S65801
A;Residues: 1-273 <BBS
A;Cross-references: UNIPROT.P20826; UNIPARC:UPI0000028C9B; EMBL:U44725; NID:g1172215; PI
R;Huang, E.J.; Nocka, K.H.; Buck, J.; Besmer, P.
Mol. Biol. Cell 3, 49-362, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit-A;Residues: 1-214, TL', 216-273 <HUD.
A;Residues: 1-224, 
                                                               cell factor - dog
C;Species: Canis lupus familiaris (dog)
C;Accession: 146929
R;Shull, R.M.; Suggs, S.V.; Langley, K.E.; Okino, K.H.; Jacobsen, F.W.; Martin, P.H.
Sxp. Hematol. 20, 118-1124, 1992
A;Title: Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic p.
A;Reference number: 146929; MUID: 93106145; PMID: 1281786
A;Accession: 146929
A;Reference preliminary; translated from GB/EWBL/DDBJ
A;Redicus: preliminary; translated from GB/EWBL/DDBJ
A;Residus: 1-274 <&HU>
A;Residus: 1-274 <&HU>
A;Residus: 1-274 <&HU>
C;Superfamily: mouse mast cell growth factor
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84.5%; Score 1180.5; DB 2; Length 274;
Best Local Similarity 85.4%; Pred. No. 1.5e-84;
Matches 234; Conservative 17; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 ROPSLTRAVENIQINEEDNEISMLOEKEREFOEV 273
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A; Accession: B35974
A; Status: preliminary
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                                                                                                                                                                                                                                                                                      61
                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                            mast cell growth factor precursor (version 2) - mouse

N;Alternate names: KL-2 protein
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37934; B43751
C;Accession: A37934; B43751
C;Al 64, 1025-1035, 1991
A;Title: Transmembrane form of the kit ligand growth factor is determined by alternative
A;Reference number: A37934; MUID:91160046; PMID:1705866
A;Accession: A37934
A;Molecule type: mRNA
A;Resion: B.J: Nocka, K.H.; Buck, J: Besmer, P.
Mol. Biol. Cell 3, 349-362, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit-A;Resion: B43751
A;Resion: A3751; MUID:9233001; PMID:1378327
A;Residues: 1-173, R.J.; Nocka: M.J.S-186, L', 188-245 < HUA>
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Noce: the authors translated the codon TTG for residue 187 as Trp
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       otem cell factor precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58313
R;McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D.
submitted to the EMBL Data Library, August 1995
A;Bescription: Molecular cloning and biological activity of ovine stem cell factor.
A;Reference number: S58313
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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1 MKKTQTWIITCIYLQLLLFNPLVKTKEICGNPVTDNVKDITKLVANLPNDYMITLMYVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.9%; Score 991; DB 2; Length 245; Best Local Similarity 72.2%; Pred. No. 7.1e-70; Matches 197; Conservative 19; Mismatches 29; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 QSSLTRAVENIQINEEDNEISMLQQKEREFQEV 273
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                                                                         241 OPSLTRAVENIQINEEDNEISMLOEKEREFOEV
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A;Cross-references: UNIPROT:P79368; UNIPARC:UPI000016C4E5; EMBL:Z50743; NID:g940807; PID.
C;Superfamily: mouse mast cell growth factor
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C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Accession: B35974; A39805

R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.

B, J.C.; Patel, A.C.; Fisher, B.F.; Brjavec, H.O.; Herrera, C.J.; Wypych, J.; Sachdev, R.

Cell 63, 203-211, 1990

A;Title: Primary structure and functional expression of rat and human stem cell factor D)

A;Reference number: A35974; MUID:91004219; PMID:2208279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-201 cAMR.
A;Residues: 1-201 cAMR.
A;Cross-references: UNIPROT: P21581; UNIPARC: UDI0000144090; GB: M59966; NID: G206661; PIDN:
R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zeebo,
C. Biol. Chem. 266, 8102-8107, 1991
A;Title: Amino acid sequence and post-translational modification of stem cell factor iso
A;Reference number: A39805; MUID:91217037; PMID:1708771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                           Query Match 63.4%; Score 885.5; DB 2; Best Local Similarity 86.1%; Pred. No. 9e-62; Matches 174; Conservative 15; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
61.3%; Score 857; DB 2;
Best Local Similarity 82.6%; Pred. No. 1.5e-59;
Matches 166; Conservative 15; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Readiues: 'E',27-190 <LUA>
A;Cross-references: UNIPARC:UF1000014F57C
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TKPFMLPPVAASSLRNDSSSSN 201
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green cell factor - human (fragments)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CiAccession: 829052
Rilu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J. Langley, K.B.
Arch. Biochem. Biophys. 298, 150-158, 1992
Arch. Biochem. Biophys. 298, 150-158, 1992
A;Title: Post-translational processing of membrane-associated recombinant human stem cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                   61 MDSLPNHCWLHLMVPEFSRSLHNLLQKFVDISDMSDVLSNYSIINNLTRIINDLMACLAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 NSSKO-LKKSPKSPBPRLFTPBBFFRIFNRSIDAFKDFVVASETSDCVVSSTL-SPEKDS 175
                                                                                                                                                           RVSVTKPFMLPPVAASSLRND-----SSSSNRKAKNPPGDSSLHWAAMALPALFSLIIG 229
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121 DKNKDFIKENGHLYEEDRFIEDENFFELFNRTIEVYKEFADSLDKNDCIMPSTVETPE--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVSVTKPPMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGAL 235
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                                                                             NSSKO-LKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASBTSDCVVSSTL-SPEKDS
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                                                                                                                                                                                                                                           PAFGALYWKKRQP-SLTRAVENIQIN--EEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                 241 FILGVIYWKKTHPKSRPESNETTQCHGCQEENBISMLQQKEKEHLQV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 253;
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45.2%; Pred. No. 1.5e-38;
ative 48; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                    stem cell factor short form precursor
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Matches 127; Conservative
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        Street cell factor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 09-Jul-2004
C;Accession: JN0637
C;Accession: JN0637
R;Zhou, J.H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A;Title: Sequence of a CDNA encoding chicken stem cell factor.
A;Reference number: JN0637; MUID:93273244; PMID:7684722
A;Reference number: JN0637
A;Molecule type: mRNA
A;Residues: 1-287 <ZHO>
A;Residues: 1-287 <ZHO>
A;Coperiemental source: brain
C;Superfamily: mouse mast cell growth factor
C;Keywords: growth factor; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <AIG>
F;26-287/Froduct: stem cell factor #status predicted <AIM>
F;26-248/Domain: transmembrane predicted <AIM>
C;Way
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Strong for precursor - quail
C; Species: Coturnix coturnix (quail)
C; Species: Coturnix coturnix (quail)
C; Species: Coturnix coturnix (quail)
C; Species: O6-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C; Accession: S70366
R; Petitte, J.N.; Kulik, M.J.
Bjochim. Blophys. Acta 1307, 149-151, 1996
A; Title: Cloning and characterization of cDNAs encoding two forms of avian stem A; Reference number: S70366; MUID:96283808; PMID:8679698
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-287 < PET>
A; Cross-references: UNIPARC:UPI000013563D; EMBL:U43078; NID:g1150875; PIDN:AAC59
C; Superfamily: mouse mast cell growth factor
C; Superfamily: mouse mast cell growth factor
C; Superfamils: signal sequence #status predicted <SIG>F; 26-287/Product: stem cell factor long form #status predicted <MAT>
F; 26-287/Product: stem cell factor long form #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVSVTKPFMLPPVAASSLRND----SSSSNRKAKNPPGDSSLHWAAMALPALFSLIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSSKD-LKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTL-SPEKDS
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                                                                                                                                                                                                                                                                                                                                                                                                     50.3%; Score 703; DB 2; Length 287; 51.9%; Pred. No. 2.3e-47; live 50; Mismatches 74; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.3%; Score 702; DB 2; Best Local Similarity 51.6%; Pred. No. 2.8e-47; Matches 148; Conservative 51; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 51.9
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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A;Reference number: S29052; MUID:92398336; PMID:1381905
A;Accession: S29052
A;Status: S29052
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
Cross-references: UNIPROT:QTM4N8; UNIPARC:UP10000179563; UNIPARC:UP10000179564; UNIPARC;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mast cell growth factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: B35971
R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, A;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, A;Frille: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971; MUID:91004215; PMID:1698553
A;Accession: B35971
A;Accession: B35971
A;Accession: B35971
A;Accession: B35971
A;Accession: B35971
A;Crosser-references: UNIPROT:P20826; UNIPARC:UP10000179562
C;Superfamily: mouse mast cell growth factor
C;Keywords: transmembrane protein
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Mast cell growth factor - mouse (fragment)

mast cell growth factor - mouse (fragment)

(Species: Nue musculus (house mouse)

(Species: Musculus (house mouse)

(Species: Musculus (house mouse)

(Species: Musculus (house mouse)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSFEPRLFTPEEPRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 DKFSNISEGLSNYSII-----DDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.3%; Score 576.5; DB 2; Length 124; Best Local Similarity 75.2%; Pred. No. 5.4e-38; Matches 124; Conservative 0; Mismatches 0; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.6%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 2.7e-07;
Matches 34; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 172.5; DB 2; Length 49; 73.5%; Pred. No. 4.4e-07;
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Best Local Similarity
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        Matches
        36;
        Conservative
        4;
        Mismatches
        6;
        Indels
        3;
        Gaps
        2;

        NY
        28
        ICRNRVIANIVKDVIKLVANLPKDYMITLKKYPGMDVLPSHCWISEMVVQ
        76

        ND
        3
        ICGNPVTDNIVKD/ITKLVANLPNDYMITLINIVAGMDVLPS--WX-DMVIQ
        48
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Search completed: February 22, 2006, 18:20:27 Job time : 23.562 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model Run on:

Pebruary 22, 2006, 18:05:51 ; Search time 140.636 Seconds
 (without alignments)
 1369.555 Million cell updates/sec

US-10-620-642-61 1397 1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQEKEREFQEV 273 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Description		z4 papio cynoc	ednne	.69 felis silve		119 capra hircu	_	20 canis famil		lz2 homo sapien			168 ovis aries	114 rattus norv	mus			.08 gallus gall	114 coturnix co	ing homo sapien	154 mus musculu		ng amphatoma m	cv0 xenopus lae	m7 xenopus lae		he brachydanio			Q56jh5 brachydanio	m4 plasmodium
	eac :	P2158	Q865z4	Q95md2	P79169	029030	Q95m19	028132	006220	095n18	Q68dz2	P21581	P20826	P79368	054a14	064384	078ed8	086419	009108	090314	Q7m4n8	0 61854	08c9k1	09ygp2	Q7zxv0	Q8ayn7	06dtw3	Q56jh6	0481a5	Q8spm7	56.	<u>38</u>
COLUMNICATION	OT.		RIM		BLCA	IG	APHI	OVIN	ANFA		HUMAN		SCF_MOUSE F									MOUSE			Q7ZXV0_XENLA	Q8AYN7_XENLA	Q6DTW3_XENLA	Q56JH6_BRARE	Q4S1A5_TETNG	CANFA	BRARE	
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	Length	273	245	274	274	274	274	274	274	274	238	273	273	267	245	208	208	164	287	287	124	123	160	271	270	270	270	272	234	36	267	1697
* Query	March	0.001	87.6	87.3	87.2	86.1	85.0			.5	8.8	82.9	82.8	82.8	0:	6:	6:1	8.	50.3	50.3	41.3	36.4	34.4	26.8	24.6	21.6	21.4	6.	۲: ٦	0.4	9.3	1.
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C	Score	1397	1224	1219.5	1217.5	1203.5	1187.5	1184.5	1180.5	1180.5	1111	1158	1157	1156.5	992	865	865	835	703	702	576.5	509	480	375	343	302	299	207.5	154.5	145	130	127
Result		-	7	m	4	2	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25	56	27	28	29	30	31

Q8mwp2 plasmodium Q8mwp1 plasmodium Q8mwh2 plasmodium Q4z43 plasmodium Q7rem0 plasmodium Q7rem0 plasmodium Q6fly9 candida gla Q75f R ashbya goss P54637 dictyosteli Q74sy3 dictyosteli Q7yxx2 cryptospori Q7yxx2 cryptospori Q97h56 clostridium Q97h56 emericella
08MWP2_PLAFA 08MWP1_PLAFA 08MMI2_PLAFA 04Z403_PLABE 07REM0_PLAYO 06FLY9_CANGA 07FY78_CANGA 07FY78_DICDI 07R0E9_PLAYO 07R0E9_PLAYO 07R0E9_PLAYO 077XXZ_CRYPV 097HS6_CLOAB
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1711 1713 1716 330 555 1011 373 989 989 989 1231 1665 5542 465
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127 127 127 116.5 109 108.5 107.5 106.5 106.5 106.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                NUCLECATION SEQUENCE OF 167-248 (ISOFORM 2).

RX MUCLECATION SEQUENCE OF 167-248 (ISOFORM 2).

RX TOYOLA M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;

RA TOYOLA M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;

RI "Expression of two types of kit ligand mRNAs in human tumor cells.";

RI Int. J. Hematol. 55:301-304(1992).

- I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid augment the proliferation of both myeloid and lymphoid coll-cell adhesion. Acts synergistically with other cytokines, or probably interleukins.

CC probably interleukins.

CC probably interleukins.

- SUBINIT: Homodimer, non-covalently linked (Probable).

- SUBINIT: Homodimer, non-covalently linked (Probable).

- SUBINIT: Homodimer, non-covalently linked (Probable).

- ALTERNATIVE PRODUCTS:

Evente-Alternative splicing; Named isoforms 1 only) (By similarity).

- ALTERNATIVE PRODUCTS:

Evente-Alternative splicing; Named isoforms=2;

Name=1; Synonyms=SCF220;

- ISOId=P21583-1; Sequence=Displayed;

- ISOId=P21583-2; Sequence=Usp 006022;

- IDEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.

- I- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.

- ISOId=P2188: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

- HOMIARIY: Belongs to the SCF family.

- HOMIARIY: Belongs to the SCF family.

- HOMIARIY: Belongs to the SCF family.

- HOMIABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;

- WWW-hittp://www.infobiogen.fr/services/choncancer/Genes/MGFID142.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bhoinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Whiting M., Madan A., Young A.C., Scherchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B., Schmutz J., Myers R.M., Schein J.B., Schantz J., Myers R.M., Schein J.B., Schalb J.B., Sones S.J.M., Marra M.A., Schein J.B., Jones J.M., Jones J.M
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GO; GO:0005173; F:stem cell factor receptor binding; NAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0030097; P:hemopolesis; NAS.
GO: GO:0007165; P:signal transduction; TAS.
InterPro; IPR012351; Cytokine 4 hlx.
                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, M59964; AAA85450.1; -; mRNA.
EMBL, AF119835; AAD22048.1; -; mRNA.
EMBL, AF400436; AAA22486.1; -; mRNA.
EMBL, AF400436; AAA22486.1; -; mRNA.
EMBL, BC406973; AA469733.1; -; mRNA.
EMBL, BC06973; AA46973.1; -; mRNA.
EMBL, BC069797; AA469791.1; -; mRNA.
EMBL, BC069797; AA469791.1; -; mRNA.
EMBL, BC074725; AA444725.1; -; mRNA.
EMBL, S42571; AAB22846.2; -; mRNA.
PIR, A35974; A35974.
PIR, B61190; B61190.
PDB; IEXZ; X-ray; A/B/C/D=26-166.
PDB; IEXZ; X-ray; A/B/C/D=26-166.
PDB; IEXZ; X-ray; A/B/C/D=26-166.
PDB; IEXZ; W-ray; A/B/C/D=273.
ENBGMDL; BNSG00000049130; HOMO Bapiens.
MIN; 184745; -
                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02404; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed.
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1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 KPFWLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAWALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KOLKKSFKSPEPRLPTPEEFFRIPNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
W 3D-structure; Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Signal; Transmembrane.

SIGNAL

SIGNAL

T SIGNAL

T SIGNAL

T SIGNAL

T TRANSNEM

T CARBOHYD

T TRANSNEM

T T TRANSN
                                                                                                                                      Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. ..) (Potential).

By similarity.

By similarity.

Fy similarity.

Fy linked (SC22).

FridevSp 066022.

I -> S (in Ref. 3 and 4; AAK92486).

K -> R (in Ref. 3 and 4; AAK92486).

L -> P (in Ref. 3 and 4; AAK92486).

L -> P (in Ref. 3 and 4; AAK92486).

L -> P (in Ref. 3 and 4; AAK92486).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1397; DB 1; Length 273; 100.0%; Pred. No. 1.7e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUCLEOTIDE SEQUENCE.

Kalina T., Storek J.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
SUBMI, AV226584; AA072537.1; -; mRNA.
HSSP; P21583; 1EXZ.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:0005173; F:stem cell factor receptor binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003452; SCF.
PEam; PP02404; SCF; 1.
SEQUENCE 245 AA; 27887 MW; 937B3CAF28D694FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
1-UNAR-2004 (TrEMBLrel. 26, Last annotation update)
Stem cell factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 55 L
128 128 K
134 134 L
273 AA; 30899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0%;
Matches 273; Conservative C
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Q86524;
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09

120

180 180 240 240 m

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240 ]
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CARBOHYD
CARBOHYD
DISULFID
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
SC COS CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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A Murray J.D., Bowling A.T.;
The proliferation of mast cells. Able to
submitted (JAN-2000) to the EMBL/GenBark/DDBJ databases.

- I- FUNCTION: Stimulates the proliferation of mast cells. Able to
augment the proliferation of both myeloid and lymphoid
hematopoietic progenitors in bone marrow culture. Mediates also
cell-cell adhesion. Acts synergistically with other cytokines,
probably interleukins (By similarity).

- SUBGELLULAR LOCATION: Type I membrane protein. Also exists as a
secreted soluble form (By similarity).

- PTMR A soluble form is produced by proteolytic processing of the
extracellular domain (By similarity).

- SIMILARITY: Belongs to the SCF family.
                                                                                                                                       MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKTVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                            MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                      MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                  KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASBTSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                                                                                                                                                            KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKG-----
                                                                                                                                                                                                                                                                                                                                                                                           KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                        ------KAKNPPGDSSLHWAAMALPAFFSLIIGFAFGALYWKKR
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin,
Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
Ran equine sequence homologous to stem cell factor (KIT-ligand).";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terry R.R., Billey B.F., Cothran B.G.; "Evaluation of MGF as the candidate gene for Appaloosa spotting. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        095MD2; 062765; 095MG7; 095MG8; 0911Y5; 28-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 10-MXY-2005 (Rel. 41, Last annotation update) Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) cell growth factor) (MGF).

Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 4-264.
Terry R.R., MicKelson J.R., Schmutz S., Cothran B.G., Bailey "Eguus caballus mast cell growth factor (MGP).", Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                   2; Indels
                   87.6%; Score 1224; DB 2;
88.6%; Pred. No. 2.4e-85;
ive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE OF 107-202 AND 227-274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPSLTRAVENIQINEDDNEISMLQEKEREFQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE OF 12-267.
                   Query Match
Best Local Similarity 88.6
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HORSE
                                                                                                                                                                                                        61
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SOF HORSE

10 — SOF HORSE

DT 28 - FEE

DT 28 - FEE

DT 10 - MAX

DE Kill 1.

DE Kill 1.

DE KIL 1.

RA NUCLE

RA RIEGE

RA R
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This Swiss-Frot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENEL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWIITCIYLQLLLFNPLVKTKGICENRVTDDVKDVKLVANLPKDYKITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENVKKSYKSOBSRLFTPERFFRIFNRSIDAFKDLEMVVSKTSECVVSSTLSPEKDSRVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TKPPMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; Growth factor; Signal; Transmembrane.
Potential.
Kit ligand.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
Q -> P (in Ref. 2).
Missing (in Ref. 3).
Missing (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCF FELCA STANDARD; PRT; 274 AA.
P79169;
28-FEB-2003 (Rel. 41, Created)
10-MAY-2003 (Rel. 47, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.3%; Score 1219.5; DB 1; Length 274; 87.2%; Pred. No. 6.2e-85; ive 19; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROPSLITRAVENIQINEEDNBISMLQEKERBFQBV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274
                                                                                                                                                                                                                 EMBL; AF401625; AAK94474.1; -; MRNA.
EMBL; AF053498; AAC97076.1; -; MRNA.
EMBL; AF367704; AAK63249.1; -; Genomic_DNA.
EMBL; AF307706; AAK62250.1; -; Genomic_DNA.
EMBL; AF1307706; AAK536716.1; -; Genomic_DNA.
EMBL; AF130770; AAK536716.1; -; Genomic_DNA.
InterPro; IPR012251; Cytokine_4_hlx.
InterPro; IPR012251; Cytokine_4_hlx.
InterPro; IPR012521; Cytokine_4_hlx.
INTERPRO; IPR01452; SCF.
PANTHER; PTHR11574; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31217
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Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
26
216
239
239
90
97
145
116
116
115
27
4 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion; G
SIGNAL
1
CCRAIN 26
TOPO DOM 26
TRANSMEM 216
TOPO DOM 239
CARBÖHYD 90
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TKPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FF3C87114D7BA6A6 CRC64;
                                                            273
                                                                             241 KQPNLTRTVENIQINEEDNEISMLQEKEREFQEV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1203.5; Di
Pred. No. 1e-83;
                                                            ROPSLTRAVENIQINEEDNEISMLOEKEREFOEV
                                                                                                                                                                  274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L07786; AAA53670.1; -; mRNA.
PIR; 146575; 146575.
BIR; Q293030; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR013452; SCF.
PANTHER; PTRAI1574; SCF; 1.
Pfam; PP02404; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94146218; PubMed=7508758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 N-
196 N-
114 By
164 By
31119 MW;
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                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 [1]
NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                                                                               and 2).
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                                                              Dunham S.P., Onions D.E.; "The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor.";
                                                                                               DNA Seq. 6:233-237(1996).

DNA Seq. 6:233-217(1996).

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoidetic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!- SUBUNIT: Homodimer, non-covalently linked (Probable).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms I and 2) Also exists as a secreted soluble form (isoform I only) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Signal; Transmebrane.
SIGNAL
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N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
By similarity.
By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR -> G (
                                                                                                                                                                                                                                                                                                                                  Isold=P79169-2; Sequence=VSP 006021; PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity). SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kit ligand.
Extracellular (Potential).
Potential.
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                                                                                                                                                                                                                                                                          Event=Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP 006021
                                                                                                                                                                                                                                                                                                        lsoId=P79169-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform 2)
                       [1]
NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D50833; BAA09445.1; -; mRNA.
SMR; P79169; 29-161.
                                                TEDLINE=97069946; PubMed=8912926;
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Matches 239; Conservative
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      WCBI_TaxID=9685;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name-KITLG; Synonyms-MGF;
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; Signal; Transmembrane.
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Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

N-linked (GloNAc. .) (Potential).

By similarity.

By similarity.
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Page 5

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NUCLECATIDE SEQUENCE.

STRAIN=Shiba; TISSUE=Brain;

A Tanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Tanagisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Tadentification of splicing isoforms of caprine stem cell factor (SCF) transcripts and expression patterns of the two major isoforms, agree of the control of superior (SCF) and SCF741, in the brain and the skin of adult and fetal shiba goats, Capra hircus.";

Shiba goats, Capra hircus.";

Shiba goats, Capra hircus.";

L. Shiba goats, Capra hircus.";

Shiba goats, Capra hircus.";

L. Shiba goats, Capra hircus.";

Shiba goats, Capra hircus.";

Shiba goats, Capra hircus.";

L. Shiba goats, Capra hircus.";

C. -- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

C. -- SUBGNIT: Homodimer, non-covalently linked (Probable).

Secreted soluble form (By similarity).

C. -- PTM: A soluble form (By similarity).

C. -- PTM: A soluble form (By similarity).

C. -- PTM: A soluble form (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TKPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK
                                                                                             MDVL.PSHCWISEMVVQL.SDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                              MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                           KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOF-VVASETSDCVVSSTLSPEKDSRVSV
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
11-MAMP-2005 (Rel. 47, Last annotation update)
12-MAMP-2005 (Rel. 47, Last annotation update)
13-MAMP-2005 (Rel. 47, Last annotation update)
14-MAMP-2005 (Rel. 47, Last annotation update)
15-MAMP-2005 (Rel. 41, Last annotation update)
16-MAMP-2005 (Rel. 41, Last annotation update)
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SMR; Q95M19; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfan; PP02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth factor; Signal; Transmembrane.
SIGNAL
   Indels
   16;
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22; Mismatches
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NCBI_TaxID=9925;
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Q95M19;
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C 028132; O9TU74;

C 28-FEB-2003 (Rel. 41, Last sequence update)

T 28-FEB-2003 (Rel. 47, Last annotation update)

T 10-MAY-2005 (Rel. 47, Last annotation update)

E Xit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast E cell growth factor) (MGF).

Name=KITLG; Synonyme=SCF;

Name=KITLG; Synonyme=SCF;

S Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

C Butaryota; Metazoa; Chordata; Craniata; Cetartiodactyla; Ruminantia;

C Pecora; Bovinae; Bos.

NRSI_TaxID=9913;
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MEDLINE=99315331; PubMed=10384045; DOI=10.1007/8003359901076;
Seitz J.J., Schmutz S.M., Thue T.D., Buchanan F.C.;
"A missense mutation in the bovine MGF gene is associated with the roan phenotype in Belgian Blue and Shorthorn cattle.";
                                                                                                                                                        (Potential). (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%; Score 1187.5; DB 1; Length 274;
85.0%; Pred. No. 1.7e-82;
tive 20; Mismatches 20; Indels 1;
Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. . .) (Pote
By similarity.

By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                      BBFE669A509EF65D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 204-239, AND VARIANT ASP-218
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Biochim. Biophys. Acta 1223:148-150(1994)
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TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                      31053 MW;
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Best Local Similarity 85.0%:
Matches 233; Conservative
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TO C2813
DT 28-PE
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180 TKPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK 239
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EMBL; AY094361; AAM16280.1; -; mRNA.
PIR; 146229; 146929.
SRR; Q06220; 29-161.
Ensembl; ENSCAPG00000006091; Canig fa
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InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PARTER: PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
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                                                                                                                                                                                                                              STANDARD;
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NUCLEOTIDE SEQUENCE.
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SCF_CANFA
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                                                                                                                                                                                                                                                                                Isola-Q28132-2; Sequence=VSP 006020; PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity). POLYMORPHISM: The roan locus is responsible for the coat coloration of Belgian Blue and Shorthorn cattle. The solid-colored and white animals are homozygotes, and the roan animals, with intermingled colored and white hairs, are heterozygous. The roan Shonthorype is due to the Asp-218 mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTQTWIITCIYLQLLFPPLVHTQGICSNRVTDDVKDVKLVANLPKDYMITLKYVPG
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Mamm. Genome 10:710-712(1999).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

-I- SUBGNIT: Homodimer, non-covalently linked (Probable).

-I- SUBCELLUAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Also exists as a secreted soluble form (isoform 1 only) (By similarity).
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(ytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
By similarity.
Companies of the companies 
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Extracellular (Potential).
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D6ClDDB77B0CB12B CRC64;
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84.7%; Pred. No. 2.9e-82;
iive 20; Mismatches 21
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EMBL; AB033716; BAA94808.1; -; mRNA.
EMBL; AF120154; AAD55355.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                 IsoId=Q28132-1; Sequence=Displayed;
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274 AA; 31015 MW;
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Best Local Similarity 84.74
Matches 232; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                            006220; QBSPM6;
01-UJN-1994 (Rel. 29, Created)
01-UJN-1994 (Rel. 29, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Canine stem cell factor (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture."; Exp. Hematol. 20:1118-1124(1992).
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Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W.,
Martin P.H.;
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COSTAIR; O95MNS;

T 28-FEB-2003 (Rel. 41, Created)

T 28-FEB-2003 (Rel. 41, Last sequence update)

T 10-MAY-2005 (Rel. 47, Last annotation update)

E Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor)

Name=KITLG; Synonyms=SCF;

Name=KITLG;

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Thm: A soluble form is produced by proteolytic processing
isoform in the extracellular domain (By similarity).
SIMILARITY: Belongs to the SCF family.
                                                                                                        4182BE9AED00793B CRC64;
Cytoplasmic (Potential).
N-linked (GlCNAc. . .) (FN linked (GlCNAc. . .) (FN shallarity.
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Name=1;
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Name=2;
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NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
                                                                                                        MW;
                                                                                                                                 Query Match
Best Local Similarity 85.4%;
Matches 234; Conservative
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
45-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686F2250.
Name=DKFZp686F2250;
Name=DKFZp686F2250;
Name=DKFZp686F2250;
Name=DKFZp686F2250;
Name=DKFZp686F2250;
Name=DKFZp686F2250;
Namemalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GloxNc. .) (Potential).

N-linked (GloxNc. .) (Potential).

N-linked (GloxNc. .) (Potential).

N-linked (GloxNc. .) (Potential).

By similarity.

By similarity.

DSRYSVTKPPMLPPVAASSLRNDSSSSNR -> G (S)
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/FTIG=VSP 006024.

S -> P (in Ref. 1, AAK73366).
S -> N (in Ref. 1, AAK73366).
EREFQEV -> RESFKRCNCGFYHTVLSYLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5AC1619014AE5E72 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    SMR; Q95NB; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; PRR012551; SCF.
PANTHER; PTR11574; SCF; 1.
Alternative splicing; Cell adhesion; G
Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                 EMBL; AY013712; AAG37434.1; -; mRNA.
EMBL; AF323757; AAK73366.1; -; mRNA.
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068D22 HUMAN PRELIMINARY;
AC 068D22;
DT 25-OCT-2004 (TrEMBLrel. 28, DT A5-OCT-2004 (TREMBLREL. 28, DT A5-OCT-204 (TREMBLREL. 28, DT A5-OCT-204 (TREMBLREL.) (TREMBLREL. 28, DT A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUCLECTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE-91004119; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
Morris C.P., MoNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher E.P., Exjavec H.O., Hearrer C.J., Wypyoh J., Sachdev R.K.,
Pope J.A., Leelle I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
"Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi;
Muridea, Muridee, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                      Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, CR749222; CAH18078.1; -; mRNA.

SMR; Q68D22; 9-126.

G0; G0:001620; G:membrane; IEA.

G0; G0:0010513; F:stem cell factor receptor binding; IEA.

G0; G0:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P21581; Q9QWZ4; Q9Z2E7;
01-MAY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLOEKEREFOEV 273
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                                                                                                                                                                                                                                                                                                                       83.8%; Score 1171; DB 2; Length 238; 100.0%; Pred. No. 2.6e-81; ive 0; Mismatches 0; Indels (
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Teramoto T., Nagashima M., Thorgeirsson S.S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Buffalo; TISSUB=Liver;
MEDLINE=91217037; PubMed=1708771;
Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren
                                                                                                                                                                                                                                                                                   238 AA; 26667 MW; 7D6B1E487BE3709B CRC64;
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                  TISSUE=Amygdala;
The German cDNA Consortium;
                                                                                                                                                                                                                    InterPro; IPR003452; SCF.
Pfam; PF02404; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                 Matches 230; Conservative
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63:203-211(1990)
                                                                                                                                                                                                                                                                  protein.
SEQUENCE.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                    Cell 63:195-201(1990).

-1- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoids augment the proliferation of both myeloid and lymphoids also hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
-1- SUBURIT. Homodimer, non-covalently linked (Probable).
-1- SUBCELLUIAR LOCATION: Type I membrane protein (isoforms 1 and 2) Also exists as a secreted soluble form (isoform 1 only) (By similarity).
                                                                                                                     PROTEIN SEQUENCE OF 26-39.
MEDLINE=91004218; PubMed=2208278; DOI=10.1016/0092-8674(90)90300-4; Zsebo K.M., Wypych J., McNiece I.K., Lu H.S., Smith K.A., Karkare S.B., Sachdev R.K., Yuschenkoff V.N., Birkett N.C., Williams L.R., Satyagal V.N., Tung W., Bosselman R.A., Mendiaz E.A.,
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"Amino acid sequence and post-translational modification of stem of factor isolated from buffalo rat liver cell-conditioned medium.";
J. Biol. Chem. 26:8102-8107(1991).
                                                                                                                                                                                                                                               Langley K.E.; "Identification, and biological characterization of hematopoietic stem cell factor from buffalo rat liver-conditioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02404; SCF; 1... Alternative splicing; Cell adhesion; Direct protein sequencing; Glycoprotein; Growth factor; Pyrrolidone carboxylic acid; Signal; Transmembrane.
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Potential.
Cytoplasmic (Potential).
Cytoplasmic (Potential).
N-linked (GlCNAc. .); partial.
N-linked (GlCNAc. .);
O-linked (Probable).
O-linked (Probable).
N-linked (Probable).
N-linked (GlCNAc. .); partial.
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/FIId=VSP 006025.
S -> P (in Ref. 1; AAD02828).
C0P56527DC93FD27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP071204; AAD02827.1; -; mRNA.
EMBL; AP071205; AAD02828.1; -; mRNA.
EMBL; M5966; AAA42117.1; -; mRNA.
EMBL; M5956; AAA42117.1; -; mRNA.
EMR, P21581; 29-159.
Ensembl; ENSRNOG0000000386; Rattus norvegicus.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR012351; CyFC, IPR012351; PMNHER; PTR11574; SCF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1; Synonyms=KL-1;
IsoId=P21581-1; Sequence=Displayed;
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30712 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                   MKKTQTWILTCIYLQLLLFNPLVKTBGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=3912240; PubMed=1383087;
Brannan C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.,
"Developmental abnormalities in Steell7H mice result from a splicing
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92330001; PubMed=1378327;
Huang E.J., Nocka K.H., Buck J., Besmer P.;
"Differential expression and processing of two cell associated forms
of the kit-ligand: XL-1 and KL-2.";
Mol. Biol. Cell 3:349-362(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91160046; PubMed=1705866; DOI=10.1016/0092-8674(91)90326-T; Flanagan J.G., Chan D.C., Leder P.; "Transmembrane form of the kit ligand growth factor is determined by alternative splicing and is missing in the Sld mutant."; Cell 64:1025-1035(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=WCB6F1;
MEDLINE=91004223; PubMed=1698558; DOI=10.1016/0092-8674(90)90304-W;
Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J.,
Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D.,
Williams D.E.;
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KL) (Steel
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                            Length 273;
                                                                                         30; Indels
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                         ;; Score 1158; DB 1;
;; Pred. No. 3.1e-80;
18; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 QSSLTRAVENIQINEEDNEISMLQQKEREFQEV 273
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                         sch 82.9%;
il Similarity 82.4%;
225; Conservative 1
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                      Query Match
Best Local S:
Matches 225
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NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC STRAIN=C57BL/61; TISSUB=Cerebellum;

RRDININ=C57BL/61; TISSUB=Cerebellum;

RRDININ=C57BL/61; TISSUB=Cerebellum;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondowa H.,

RA Aladarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Marapin A., Fletcher C.F., Forrest A., Gough J.,

Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,

RA Balta B., Dragani T.A., Fletcher C.F., Forrest A., Gough J.,

RA Gassterland T., Cariboldi M., Gissi C., Godzik A., Gough J.,

RA Gassterland T., Marain I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Gasterland T., Nunata R., Pottius J., McKenzie L., Miki H.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Rayashima T., Nunata R., Pontius J.U., Qi D., Ramachandran S.,

Rayashima T., Nunata K., Pontius J.U., Qi D., Ramachandran S.,

RA Sultana R., Fasenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Magner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Sultana R., Takenaka T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani V., Ishaya R.,

RA Hara A., Hashizume W., Materston R., Lander E.S., Rogers J.,

Ra Birney E., Hayashizaki Y.;

Ra Malyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa I.,

Ra Malyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa E.,

Ra Malyazaki A., Sakai K., Sasaki D., Sasaki D., Satoki M.,

Ra Malyazaki A., Sakai K., Sasaki D., Sasaki D., Sasaki D., Satoki S.,

Ra Malyazaki A., Sakai K., Sasaki D., Satoki S.,

Ra Malyazaki A., Sakai K., Sasaki D., Satoki S.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98025115; PubMed=9360640; DOI=10.1016/S1383-5726(97)00005-8; Graw V., Neuhauser-Kilaus A., Pertschi W.; Potection of a point mutation (A to G) in exon 5 of the murine Mgf gene defines a novel allele at the Steel locus with a weak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [6]
NUCLECTIDE SEQUENCE (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207.
STRAIN-C3H/B1; TISSUE-Brain,
STRAINE-31/2132534; PubMed=8875893; DOI=10.1007/8003359900247;
Graw J., Loceter J., Neuhaeuser-Klaus A., Pretsch W., Schmitt-John "Molecular analysis of two new Steel mutations in mice shows a transversion or an insertion.";
Mamm. Genome 7:843-846(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND
                                                                                                                                                                                                                                                                      Bedell M.A., Copeland N.G., Jenkins N.A.;
Multiple pathways for Steel regulation suggested by genomic and
sequence analysis of the murine Steel gene.";
Genetics 142:927-934 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1), AND VARIANT
in the steel factor cytoplasmic tail.";
                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=97002551; PubMed=8849898
                                                                                          [5]
NUCLEOTIDE SEQUENCE (ISOFORM 1)
                                             Genes Dev. 6:1832-1842(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenotype.";
Mutat. Res. 382:75-78(1997)
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Pecora; Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                       82.8%;
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                                                                                                                                                                                                                                                                                                        Matches 226; Conservative
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       M59915;
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villanon D.K., Muzny D.M., Sodergren E.J., Lux K., Gibbs R.A., Fahey J., Helton E., Ketteman M. Madan A. Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I. Schmatz J., Salaska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE OF 26-53.

MEDLINES-91004-216; PubMed=1698554; DOI=10.1016/0092-8674(90)90298-S;

MEDLINES-91004-216; PubMed=1698554; DOI=10.1016/0092-8674(90)90298-S;

COPEDIAND N.G., Gilbert D. J., Cho B.C., Donovan P.J., Jenkins N.A.,

COSEMAN D., Anderson D., Lyman S.D., Williams D.E.;

"Mast cell growth factor maps near the steel locus on mouse chromosome il on dis deleted in a number of steel alleles.";

Coll 63:175-183(1990)
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91004221; PubMed=1698557; DOI=10.1016/0092-8674(90)90303-V; Huang E., Nocka K., Beier D.R., Chu T.Y., Buck J., Lahm H.W., Welliner D., Leder P., Besmer P.; "The hematopoletic growth factor K. is encoded by the Sl locus and is the ligand of the c-kit receptor, the gene product of the W locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUCLEOTIDE SEQUENCE OF 1-201.
MEDLINE=91004220; PubMed=1698556; DOI=10.1016/0092-8674(90)90302-U; Z8ebO K.M., Williams D.A., Gelseler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hsu R.-Y., Elrkett N.C., Okino K.H., Murdock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattanach B.M., Galli S.J., Sugss S.V.;
"Stem cell factor is encoded at the Sl locus of the mouse and is the ligand for the c-kit tyrosine kinase receptor.";
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Cell 63:167-174(1990).

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoletic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
-I- SUBJUNT: Homodimer, non-covalently linked (Probable).
-I- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Also exists as a secreted soluble form (isoform 1 only) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL PROTEIN SEQUENCE OF 26-78.
MEDLINE=91004215; PubMed=1698553; DOI=10.1016/0092-8674(90)90297-R; Williams D.E., Eisenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Marthu S., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.; "Identification of a ligand for the c-kit proto-oncogene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-2; Symonyms=KL-2;
Isold=P20826-2; Sequence=VSP 006023;
DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
PTM: A soluble form is produced by proteolytic processing of
                                                                                                                                                                                                                                                                                                                                     NUCLECTIDE SEQUENCE OF 1-270 (ISOFORM 1), AND PROTEIN SEQUENCE
                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing, Named isoforms=2;
Name=1; Synonyms=KL-1;
IsoId=P20826-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoform 1 in the extracellular domain. SIMILARITY: Belongs to the SCF family.
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MDVLPSHCWLRDMVIQLSLSLTTLLDKPSNISEGLSNYSIIDKLGKIVDDLVLCMEENAP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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SUBUNIT: Homodimer, non-covalently linked (Probable).
SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P79368; Q28591;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAX-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast call growth factor) (MGF) (Fragment).
Name=KiTLG; Synonyms=SCF;
Ovis aries (Sheep).
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MEDLINE=99263397; PubMed=10328863; DOI=10.1006/cytc.1998.0430;
MEDLINE=99263397; PubMed=10328863; DOI=10.1006/cytc.1998.0430;
MEDLINE=99263397; PubMed=10328863; DOI=10.1006/cytc.1998.0430;
"The cloning and expression of the cDNA for ovine stem cell factor (kit-ligand) and characterization of its in vitro haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia;
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MEDLINE-56413880; PubMed-8662240; DOI=10.1007/8003359900142;
Tisdall D.J., Quirke L.D., Galloway S.M.;
"Oyine stem cell factor gene is located within a syntenic group chromosome 3 conserved across mammalian species.";
Mamm. Genome 7:472-473(1996).
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                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                    Length
L; M7647; AAA39538.1; -; mRNA.
L; S40534; AAB22555.2; -; mRNA.
L; V66989; CA AG4778.1; -; mRNA.
L; U4724; -; NOT ANNOTATED COS; Genomic_DNA.
L; U4725; AAC52447.1; -; mRNA.
L; X95381; CAA64667.1; -; mRNA.
L; X9532; CAA67698.1; -; mRNA.
L; X10287; CAA71329.1; -; mRNA.
                                                                                                                                                                                                                                                                                                 Score 1157; DB 1;
Pred. No. 3.7e-80;
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                                                                                                                                                                                                                                                                                                                                                                19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA
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61 MDVLPSHCWLRDMVTHLSVSLTTLLDKPSNISEGLSNYSIIDKLGKIVDDLVACMEBNAP 120
                                                                                                                                                                                                                                                                                                                     MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                    KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWIITCIYLQLLLFNPLVKTQBICRNPVTDNVKDITKLVANLPNDYMITLNYVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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[1]
NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
NUCLECTION TISSUB-Embryonic kidney;
MEDLINE=22831116, PubMed=12951073; DOI=10.1016/j.bbrc.2003.08.025;
Hirokawa Y.S., Watanabe M., Shiraishi T.;
"The 3'UTR of stem cell factor suppresses protein expression from cotransfected vector.";
                                                                                                                                                                                                                   28;
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61.9%; Score 865; DB 2; Length 208;
Best Local Similarity 82.8%; Pred. No. 5.2e-58;
Matches 169; Conservative 16; Mismatches 19; Indels
                                                                                                                                                                               Query Match 71.0%; Score 992; DB 2; Length 245
Best Local Similarity 71.8%; Pred. No. 1.3e-67;
Matches 196; Conservative 18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
C-kit ligand C-terminally truncated secreted form KL-Sld.
Name=Kitl;
                                                                                                             Biochem. Biophys. Res. Commun. 309:469-474(2003).
EMBL; AB105879; BAC84980.1; -; mRNA.
SEQUENCE 245 AA; 27681 MW; 9615130876AC9D52 CRC64;
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SEQUENCE 208 AA; 2:
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                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                   Growth factor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
(Potential).
(Potential).
secreted soluble form (By similarity).

PTM: A soluble form is produced by proteolytic processing of extracellular domain (By similarity).

SIMILARITY: Belongs to the SCF family.
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                                                                                                                                                                                                                                                                                                                             Fotential.

Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GloNAc. .) (Pote
N-linked (GloNAc. .) (Pote
N-linked (GloNAc. .) (Pote
N-linked (GloNAc. .) (Pote
By similarity.
By similarity.
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Last annotation update)
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85.0%; Pred. No. 3.9e-80;
ive 19; Mismatches 20
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SMR; P79368; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth fa
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EMBL; Z50743; CAA90620.1; -; mRNA.
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O54A14;
13-SEP-2005 (TrEMBLrel. 31, C.
13-SEP-2005 (TrEMBLrel. 31, L.
13-SEP-2005 (TrEMBLrel. 31, L.
Stem cell factor KL-2.
Name=scf;
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Matches 227; Conservative
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Search completed: February 22, 2006, 18:19:21 Job time : 141.636 secs

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 273; Conservative
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LOCATION:
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9394, Ap
                                                                     February 22, 2006, 18:19:42; Search time 33.0909 Seconds (without alignments) 682.074 Million cell updates/sec
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                                                                                                                                 1 MKKTOTWILTCIYLQLLLFN.....NEEDNEISMLQEKEREFQEV 273
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/cgn2_6/ptodata/1/iaa/FCOMB.pep:*
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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3-08-482-918-48
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US-08-482-918-61
US-09-224-681-61
US-09-324-681-61
US-08-336-728A-49
US-08-336-728A-61
US-09-635-251-49
US-09-635-251-61
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US-09-604-325A-50
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          GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Patent No. 5525708
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER INTEGRALE DIAMETICA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B
FILING DATE: 28-MAR-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
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100.0%; Pred. No. 4.9e-134;
iive 0; Mismatches 0;
US-08-336-728A-50
US-08-955-848A-82
US-08-224-681-57
US-09-235-221-57
US-09-635-221-57
US-09-635-221-57
US-09-604-325A-57
US-09-604-325A-57
US-09-224-681-63
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US-09-949-016-9392
US-09-949-016-9392
US-09-949-016-9392
US-09-949-016-9392
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XOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKOSRVSVT 180
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KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                             181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTONERY/AGRAT INPOMBATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPRENCE/DOCKET NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0480
                                                                                                                                                                                                                                      241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
                                                                                                                                                                                                           241 OPSLTRAVENIQINEEDNEISMLOEKEREFOEV 273
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APPLICANT: Zeebo, Krisztina M.
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: 111inois
COUNTX: United States of America
ZIP: 6060-6402
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/08482918 Patent No. 6207417
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 273; Conservative
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1-248 SCF protein begins at amino acid 26; amino acid 1-25
include Met and leader sequences for membrane band form of
recombinant SCF."
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                                61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                           KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIGFAFGALYWKKR 240
                                                                                                                                  KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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GENERAL INFORMATION:

APPLICANT: Lu, Haieng

TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS

NUMBER OF SUCENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSE: Amagen Inc.

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION NUMBER: US/08/628,428
FILING DATE: 05-APR-1996
CLASSIFICATION NUMBER: 35,846
REGISTRATION NUMBER: 36,846
REFERENCE/DOCKET UNBER: 3-400
INFORMATION FOR EQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: Amino acids
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Best Local Similarity 100.
Matches 273; Conservative
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LOCATION: 1..273
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                                        181 KPFMLPPVAASSLRNDSSSNRKAKNPPGDSSLHWAAMALPALFSLIGFAFGALYWKKR 240
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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APPLICANT: Zsebo, Krisztina M.
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE: AADRESSE:
ARBERT: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago Sears Tower, 233 South Wacker Drive STATE: Illinois COUNTRY: United States of America 21P: 60606-6402 COUNTRY: United States of America 21P: 60606-6402 COMPUTER READBAIL FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,918 FILING DATE: US/08/482,918 FILING DATE: US/08/482,918 FILING DATE: US/08/4810N: APAGE: CLOUGH, David W. REGISTRATION NUMBER: 36,107 REFERENCE/DOCKET NUMBER: 01017/33005 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION INFORMATI
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acids
TOPOLOGY: linear
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14 APPLICANT: Sobseland Noch: Taracia in the Sequence 91 APPLICANT: Sobseland Noch: APPLICANT: OF STRUMNICANERS: 104 APPLICANT: APPLI
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US-09-24-681-61

Sequence 61, Application US/09224681

Patent No. 2507454

GENERAL INFORMATION:

APPLICANT: Bosselam, Robert A. APPLICANT: Bosselam, Robert A. APPLICANT: Bosselam, Robert A. APPLICANT: Bosselam, Robert A. APPLICANT: Martin, Francis H. TITLE OF INVENTION: Wethod for Enhancing the Efficiency of Gene TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide COMPESSEE Marshall, O'Toole, Geretein, Murray & Borun STREET: Gaio Sears Tower, 233 South Wacker Drive COMPESSEE Marshall, O'Toole, Geretein, Murray & Borun STREET: Chicago Sears Tower, 233 South Wacker Drive COMPUTER REDABLE FORM: Marchael Floppy disk COMPUTER REDABLE FORM: Wacker Drive COMPUTER REDABLE FORM: Wacker Drive COMPUTER REDABLE FORM: WAS STREET: Good 6-6402

COMPUTER REDABLE PARCHILL Release #1.0, Version #1.30

COMPUTER REDABLE PARCHILL Release #1.0, Version #1.30

COMPUTER REDABLE PARCHILL RELEASE OF O'OF 993

SOFTWARE PARCHICATION DATA: APPLICATION NUMBER: 09/05, 993

CLASSIFICATION NUMBER: 09/05, 993

FILING DATE: 12-0AN-1995

FILING DATE: 12-0AN-1995

FILING DATE: 01-0CT-1990

PRIOR APPLICATION NUMBER: 07/59,701

FILING DATE: 11-0AN-1999

FILING DATE: 11-0AN-1990

FILING DATE: 
                                                                                                                                                                                                               KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Sequence 48, Application US/08336728A

Setent No. 6207802

GENERAL INFORMATION:
APPLICANT: Seebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STREET: 111nois
COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: In More Compatible
COMPUTER REAABLE FORM:
MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEFAULT POLICE A.
SOFTWARRE DEFAULT POLICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1397; DB 2; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRICH APPLICATION DATA:
APPLICATION UNMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 OPSLIRAVENIQINEEDNEISMLQEKEREFQEV 273
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APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMINICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                               ; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acide
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-224-681-61
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,728A
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-JUN-1990
RIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY AGENT INFORMATION:
NAME: Clough, David W.
REFERENCE/DOCKET NUMBER: 01017/32956
TELECOMMUNICATION INFORMATION:
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 273 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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US-08-336-728A-61
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South Wacker Drive
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100.0%; Score 1397; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.9e-134;
Matches 273; Conservative 0; Mismatches 0;
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PILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
PILING DATE: 07/573,616
FILING DATE: 24-AuG-1990
PRIOR APPLICATION DATA: 07/573,198
FILING DATE: 11-0UN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-0UN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1989
ATYCNEY/AGENT INFORMATION:
NAME: Clough, David M.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
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Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Buggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-336-728A-48
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US-08-336-728A-49
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                                                                                                                                                                                                                                                                                                                            121 KOLKKSPKSPERPRIFTPERFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                    61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0; Indels 0.
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SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 49:
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APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
NUMBER OF SEQUENCES: 104
ADDRESPONDENCE ADDRESS:
ADDRESPONDENCE Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6100 Sears Tower, 233 South Wacker Drive
                                                                                         ADDIGESSE: Malbidil, Oloole, Street Drive CITY: Chicago Sarks Tower, 233 South Wacker Drive CITY: Chicago STREET: 111hnois CUNTRY: United States of America 21P: 60606-6402 CONTRY: United States of America 21P: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYER: F3-0999 disk COMPUTER READABLE FORM: PC-DOS/MS-DOS OPERATIOS SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/336,728A FILING DATE: 09-NOV-1994 CLASSIFICATION NUMBER: 07/982,255 FILING DATE: 10-007-992 PRIOR APPLICATION NUMBER: 07/982,255 FILING DATE: 10-007-990 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/593,616 FILING DATE: 10-007-990 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/537,198 FILING DATE: 10-007-990 PRIOR APPLICATION NUMBER: 01017/32956 TRING APPLICATION NUMBER: 01017/32956 TRILEPHONE: 312/474-6300 TELEPHONE: 312/474-6300 TELEPHONE: 312/474-6448
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INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-336-728A-61
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| Sequence 49, Application US/0963521|
| Packett No. 675231|
| Sequence 49, Application US/0963521|
| Packett No. 675231|
| Sequence 49, Application US/0963521|
| Sequence 40, Application US/0963521|
| ITILE OF INVESTION: Stem Cell Packet
| CORRESPONDED LODGESS: O'TO Sequence | Corresponded Loggest | Corresponded Logg

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121 KOLKKSPEKPERPERPERPERPRIENTSIDAPKOPVVASETSDCVVSSTLSPEKOSRVSVT 180
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                                                                                                                                                                                        KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                              Gaps
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GENERAL INFORMATION:
APPLICANT: Seebo, Krisztina M.
APPLICANT: Suces, Sidney W.
APPLICANT: Busselman, Robert A.
APPLICANT: Busselman, Robert A.
APPLICANT: Busselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 0.04
CORRESPONDENCE ADDRESS: 3.04
CORRESPER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
CITY: United States of America
STREET: Illinois
COUNTRY: United States of America
COMPUTER READALLS FORM:
COMPUTER READALLS FORM:
COMPUTER IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/224,683
                                                                                                   Length 273;
                                                                                                Query Match
100.0%; Score 1397; DB 2; Length;
Best Local Similarity 100.0%; Pred. No. 4.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 OPSLITRAVENIOINEEDNEISMLOBKEREFOEV 273

    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-635-251-61

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APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 2-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
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US-09-224-683-49
; Sequence 49, Application US/09224683
; Patent No. 6841147
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
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181 KPFMLPPVAASSLRNDSSSSNRKAKONPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                        121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKOSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRESTORDISTEE: Marball, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STATE: 111inois
STATE: 111inois
COUNTRY: United States of America
ZIPE 66066-6402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/635,251
FILING DATE: 07-Aug-200
CLASSIPICATION NUMBER: 08/449,182
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 07/982,255
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 01-OCT-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 01-OCT-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 01-OCT-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/589,701
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/527,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTONISH DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTONISH DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                    241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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REFERENCE/DOCKET NUMBER: 01017/32957A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61, Application US/09635251
Patent No. 6759215
GENERAL INFORMATION:
APPLICANT: Zgebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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Sequence 61, Application US/09224683

Fatent No. 6841147

GENERAL INFORMATION:
APPLICANT: Sebo, Krisztina M.
APPLICANT: Suges, Sidney V.
APPLICANT: Busselman, Robert A.
APPLICANT: Busselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Srem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: 3 South Wacker Drive
CITY: Chicago
STRET: 111inois
COUNTRY: United States of America
ZIP: 6666-6402
COUNTRY: United States of America
ZIP: GO66-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BRADABLE FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 4.9e-134;
Matches 273; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,107
3R: 01017/35136
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-6300
TELEFAX: 312/474-6448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acide

TYPE: amino acide

TYPE: amino acide

TYPE: amino acide
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TOPLOGY: linear
MOLECULE TYPE: protein
US-09-224-683-49
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121 KOLKKSFKSPEPRLFTPERFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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US-09-604-325A-49
; Sequence 49, Application US/09604325A
; Patent No. 6852313
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIPICATION NUMBER: 09/449,653
FILING DATE: 2-JAN-1995
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 2-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 01017/3:
TELEPHONE: 312/474-6300
TELEPRAK: 25-3856
INPORMATION POR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 27-3 mainto acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 273 amino acids
amino acid
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RESULT 15
US-09-604-325A-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                              CITY: 1010 Sears Tower, 233 South Wacker Drive CITY: 1011cago STATE: 111inois COUNTRY: United States of America COUNTRY: United States of America ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/604,325A FILING DATE: 17-Jun-2002
CLASSIFCATION - UNICHOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,198
                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPSLTRAVENIQINBEDNEISMLOEKEREFQEV 273
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REGISTRATION NUMBER: 36,107
REPERRINCE/DOCKET NUMBER: 01017/32953
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPASS: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; INFORTH: 273 amino acids
; TYPE: amino acid STRANDEDNESS: single
; FOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-604-325A-49
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 11-JUN-1990
APPLICATION WINGBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1397; DB 2; Length 273; Best Local Similarity 100.0%; Pred. No. 4.9e-134; Matches 273; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                              NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 01017/32953
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPRAK: 312/474-0448
                                                                       Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TOPOLOGY: linear
1 MOLECULE TYPE: protein
2 SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-604-325A-61
Sequence 61, Application US/09604325A Patent No. 6852313 GENERAL INFORMATION:
                                                     APPLICANT: Zsebo, Krisztina M.
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 273 amino TYPE: amino acid
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Search completed: February 22, 2006, 18:21:59 Job time : 34.0909 secs

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REFERENCE/DOCKET NUMBER: 01017/34465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-005-243-49
February 22, 2006, 18:20:42; Search time 109.05 Seconds (without alignments) 1046.014 Million cell updates/sec
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1 MKKTQTWILITCIYLQLLLFN......NEEDNEISMLQEKEREFQEV 273
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Biocceleration Ltd.
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US-09-224-683-41
US-09-224-683-49
US-09-224-683-49
US-10-175-608-49
US-10-175-608-49
US-10-175-608-48
US-09-224-683-48
US-09-224-683-48
US-09-224-683-50
US-09-224-683-63
US-09-224-683-63
US-09-224-683-63
US-09-175-608-53
US-10-175-608-53
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US-09-005-243-51
US-09-224-683-51
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                    GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Bed
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Perfect score:
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No.
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Sequence 55, A
Sequence 55, A
Sequence 4, Ap
Sequence 55, A
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Sequence 53,
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Sequence 42,
Sequence 42,
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Sequence
Sequence
Sequence
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Sequence
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j Sequence 49, Application US/09005243

j GENERAL INFORMATION:
 j APPLICANT: Sugga, Sidney V.
 j APPLICANT: Bosselman, Robert A.
 j APPLICANT: Martin, Francis H.
 j TITLE OF INVENTION: Stem Cell Factor
 j NUMBER OF SEQUENCES: 104
 CORRESPONDENCE S. 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Gloo Seare Tower, 233 South Wacker Drive CITY: Chicago
 STAFE: Illinois
 COUNTRY: United States of America
 CONDITER: READABLE FORM:
 MEDIUM TYPE: FIRM PC Compatible
 COMPUTER: IBM PC Compatible
 COMPUTER: IBM PC Compatible
 COMPUTER: IBM PC Compatible
 COMPUTER: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/09/005,243
 FILING DATE:
 CLISCIPATION ADTA:
 APPLICATION NUMBER: US/09/005,243
US-10-175-608-51
US-10-620-642-51
US-09-005-234-631-52
US-09-224-681-52
US-09-005-24-681-53
US-09-005-24-681-53
US-09-005-24-681-53
US-09-224-681-53
US-09-224-681-53
US-09-224-681-53
US-09-224-681-55
US-09-24-681-55
US-09-24-681-55
US-09-24-681-55
US-09-24-681-55
US-09-005-241-55
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PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPTCATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILTCIYLQLLLFRNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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gequence 61, Application US/09005243

APPLICANT: Bosechman, Robert A.
APPLICANT: Bosechman, Robert A.
APPLICANT: Bosechman, Francis H.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marbhall, O'Toole, Gerstein, Murray & Borun STREET: 61300 Sears Tower, 233 South Wacker Drive CUNTRY: United States of America
STATE: 111inois
COUNTRY: United States of America
COUNTRY: United States of America
STATE: 1180Ppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/005,243
FILING NATE.
                                                                                                                                                                                                                                                                                 DB 3; Length 273;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1397; DB 3; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
TELEX: 25-3856
TELEX: 25-3856
TELEX: 25-3856
TELEX: 25-3856
TEMENT: 273 amino acids
TYPE: Alinear
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Sequence 49, Application US/09224683;
Fatent No. US20020031491A1
GENERAL INFORMATION:
APPLICANT: Zebol, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Busselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
VUMBER OF SEQUENCES: 104
CORRESOUNDENCE ADDRESS:
CORRESOUNDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1397; DB 3; Length 273; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DAVIG W.
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 273 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-005-243-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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US-09-224-683-49
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GENERAL INCORDATION:

APLICANT: Bosselman, Robert A. ADDRESS:

CORREST: 6300 Sears Tower, 233 South Wacker Drive CORREST: 6300 Sears Tower, 233 South Wacker Drive CORREST: 6300 Sears Tower, 233 South Wacker Drive CORREST: 1111nois STREET: 10509 449, 653 TILING DATE: 12-JAN-1998

COMPUTER: READLE CATION NUMBER: 09/49,653 TILING DATE: 12-JAN-1998

CLASSIFICATION NUMBER: 07/593,616

FILING DATE: 11-JAN-1990

PRIOR APPLICATION NUMBER: 07/593,616

FILING DATE: 11-JAN-1990

FILING DATE: 11-JAN-19
                 Sequence 61, Application US/09224683
Patent No. US20020031491A1
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Matches 273; Conservative
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MOLECULE TYPE: protein
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100.0%; Score 1397; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 8.5e-122;
Matches 273; Conservative 0; Mismatches 0; Indels 0;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPECATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-MOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 22-MOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 12-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-COT-1999
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-COT-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-COT-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-COT-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-CONTING NUMBER: 07/422,383
FILING DATE: 16-CONTING NUMBER: 07/424,6300
TELERDOME: 312/44-6300
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-09-224-683-49
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 9 1 MKKTQTWILITCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 100.0%; Score 1397; DB 3; Length 273; 100.0%; Pred. No. 8.5e-122; ive 0; Mismatches 0; Indels 0 셤 ò

US-09-224-683-61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASRTSDCVVSSTLSPEKDSRVSVT 180
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CORRESPONDENCE MADDRESS:
COURTS: G300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: RADDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/75,608
FILING DATE: 16-Oct-2002
CLASSIFICATION AUMBER: 09/635,249
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 10-ARW-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-ARW-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-ARW-1991
APPLICATION NUMBER: 07/593,701
FILING DATE: 10-ARW-1991
APPLICATION NUMBER: 07/573,616
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                                                                                                                                                               Length 273;
                                                                                                                                                                                                            0; Indels
                                                                                                                                                               Query Match 100.0%; Score 1397; DB 4; Best Local Similarity 100.0%; Pred. No. 8.5e-122; Matches 273; Conservative 0; Mismatches 0;
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Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61, Application US/10175608
Publication No. USZ0040181044A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
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US-10-175-608-49
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US-10-175-608-61
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CIT: Chicago
STRET: 6300 Sears Tower, 233 South Wacker Drive
CIT: Chicago
STRET: Ilinois
CONDTRY: United States of America
ZIP: 60606-6402
COMPUTER: INP FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: PATENTING SYSTEM: 16-Oct-2002
CLASSIFICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION NUMBER: 09/635,249
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 09/486,546
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/982,255
FILING DATE: 10-APPL: 1991
APPLICATION NUMBER: 07/533,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/534,019
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/534,046
                                                                                                                                                                                                                                                                                      OPSLTRAVENIQINGEDNEISMLOEKEREFOEV 273
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Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10175608
Publication No. USZO040181044A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312/474-6300
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US-10-175-608-49
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61 MDVLPSHCWISEMVVQLSDSLIDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDVLPSHCW1SEMVVQLSDSLTDLLDKFSN1SEGLSNYS11DKCVN1VDDLVECVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
                                     APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
PILING DATE: 10-0ct-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAX-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-OUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-OUN-1990
APPLICATION NUMBER: 07/422,383
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/10620642; Publication No. US20050080250A1; GENERAL INFORMATION: X=60, Krisztina M. Bosselman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                          PRIOR APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-620-642-49
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US-10-620-642-61
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Publication No. US20050080250A1
GENERAL INFORMATION:
APPLICANT: Zebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVERTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER MARFAll, O'Toole, Gerstein, Murray & Borney STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
ZIP: 66060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1397; DB 4;
; Pred. No. 8.5e-122;
0; Mismatches 0;
PILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAYIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 30,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELEPONE: 312/474-6300
TELEPAX: 312/474-648
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 273; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-175-608-61
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US-10-620-642-49
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WS-09-005-243-48

/ Sequence 48, Application US/09005243

/ APPLICANT: Zeabo, Krisztina M. APPLICANT: Sugge, Sidney V. APPLICANT: Sugge, Sidney V. APPLICANT: Martin, Francis H. TITLE OF INVENTION: Stem Cell Factor NUMBER OF SEQUENCES: 104

/ CORRESPONDENCE ADDRESS: 04

/ CORRESPONDENCE ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402

/ COUNTRY: United States of America ZIP: 60606-6402

/ COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC-COMPATA: Ploppy disk COMPUTER: BM PC-COMPATA: PAPPLICATION NUMBER: US/09/005,243
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                                                                                                                                           241 QPSLTRAVENIQINEEDNBISMLQEXEREFGEV 273
                                                                                                                 241 OPSLIRAVENIQINEEDNEISMLOEKEREFOEV
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PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
RIGH APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.64;
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MOLECULE TYPE: protein
US-09-005-243-48
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Best Local Similarity
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                                                                        CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CTTY: Chicago.
STREET: 6300 Sears Tower, 233 South Wacker Drive CTTY: Chicago.
STREET: 1111nois
COUNTRY: Illinois
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100.0%; Score 1397; DB 5; Length 273;
Best Local Similarity 100.0%; Pred. No. 8.5e-122;
Matches 273; Conservative 0; Mismatches 0; Indels 0.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: 61: US-10-620-642-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 273 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Best Local Similarity 99.6%; Pred. No. 2.5e-121;
Matches 272; Conservative 0; Mismatches 1;
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Publication No. US20040181044A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                            01017/35136
                                                                                                           REFERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELERION 312/474-6300
TELERION 312/474-6300
TELERION 312/474-6300
TELERION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: 11near
                                                                                  36,107
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-09-224-683-48
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                                                                                                                        1 MKKTQTWILTCIYLQLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zsebo, Krisztina M.
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
    1; Indels
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APPLICATION NUMBER: US/09/224,683
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01-OCT-1990
PRIOR APPLICATION NUMBER: 01-OCT-1990
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Sears Tower, 233 South CITY: Chicago STATE: 1111nois COUNTRY: United States of America ZIP: 6060-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPUTER: DOS COMPUTER: OF COMPUTER: OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/09224683; Sequence 48, Application US/09224683; Patent No. US20020031491A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
272; Conservative
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Matches
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TELEFAX: 312/474-0448
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ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-DCT-1991
APPLICATION NUMBER: 07/53,616
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/53,196
FILING DATE: 10-OCT-1990
APPLICATION NUMBER: 07/53,196
FILING DATE: 16-OCT-1999
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIGHW.
REGISTRATION NUMBER: 36,107
TELEFAX: 312/474-6300
TELEFAX: 312/474-6300
TELEFAX: 312/474-6300
TELEFAX: 312/474-6300
TELEFAX: 312/474-6300
TELEFAX: 10-000
TYPE: protein

MOLECULE TYPE: protein

WOLECULE TYPE: protein

US-10-175-608-48

ON MARMATCHES

ON MARMATCHES
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Publication No. US20050080250A1

GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Sugge, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
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US-10-620-642-48
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KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFICATION NUMBER: US/10/175,608
FILING DATE: 16-Jul-2003
CLASSIFICATION NUMBER: 09/635,249
FILING DATE: 16-CL-2002
APPLICATION NUMBER: 09/635,249
FILING DATE: 21-DC-1995
APPLICATION NUMBER: 09/172,329
FILING DATE: 21-DC-1993
APPLICATION NUMBER: 09/80,555
FILING DATE: 21-DC-1993
APPLICATION NUMBER: 09/80,701
FILING DATE: 10-ARN-1995
APPLICATION NUMBER: 09/509,701
FILING DATE: 10-ARN-1991
APPLICATION NUMBER: 09/509,701
FILING DATE: 10-ARN-1991
APPLICATION NUMBER: 09/509,701
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 09/509,701
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 09/50,303
APPLICATION NUMBER: 09/50,303
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/50,303
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPSLIRAVENIOINEEDNEISMLOEKEREFOEV 273
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-620-642-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50, Application US/09224683
| Sequence 50, Application US/09224683
| Sequence 50, Application US/09224683
| Fatten No. USZ0020031491A1
| GANRAL INFORMATION:
| APPLICANT: Boselman, Robert A. APPLICANT: Bugse, Sidney V. APPLICANT: Bugse, Sidney V. APPLICANT: Wartin, Francis H. Information: Stem Cell Factor: Composition Claims CONGRESSERS: Marchall, O'Toole, Geretein, Murray & Borun STREET: G300 Sears Tower, 233 South Wacker Drive CONGRESSERS: Marchall, O'Toole, Geretein, Murray & Borun STREET: Chicago STREE: Marchall, O'Toole, Geretein, Murray & Borun CONGRESSERS: Marchall, O'Toole, Geretein, Murray & Borun STREET: Chicago STREE: Ploppy disk COMPUTER: Inst P.Compatible COMPUTER: Barcentin Release #1.0, Version #1.30
| COMPUTER: Law P.Compatible COMPUTER: Barcentin Release #1.0, Version #1.30
| COMPUTER: Barcentin Release #1.0, Version #1.30
| CHASSISTICATION NATA: BAPLICATION NATA: APPLICATION NATA: BAPLICATION NATA: APPLICATION NATA: BAPLICATION NATA: BAPLIC
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US-09-224-683-50
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                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
STREET: G300 Gears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Unitnois
COUNTRY: United States of America
ZIP: 6606-6402
COMPUTER READBLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,243
FILING DATE: 24-MAY-1995
CLASSIFICATION:
RIOR APPLICATION STA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 25-MOV-1995
CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 2-MAY-1996
FILING DATE: 10-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-OCT-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 10-OCT-1990
PRIOR APPLICATION NUMBER: 07/422,383
APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT INFORMATION:
NAME: Clouch DATA:
APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT INFORMATION:
NAME: Clouch DATA:
ANDWET: Clouch WATA:
ANDWET: CLOU
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                                                  Sequence 50, Application US/09005243
; Patent No. US2002001018763A1
; GENERAL INFORMATION:
APPLICANT: Zeabo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01017/34465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acre
STRANDEDNESS: single
mannarOGY: linear
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MOLECULE TYPE: protein
                       US-09-005-243-50
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Search completed: February 22, 2006, 18:26:55 Job time : 109.05 secs
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                                                                                                                                                                                                                                                                                                                                                  98.9%; Score 1381; DB 3; Length 273; 98.9%; Pred. No. 2.7e-120; tive 0; Mismatches 3; Indels
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STATE: 11linois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-00c_2002
CLASSIFCATION: CUNKOWD>
PRIOR APPLICATION DATA:
APPL
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US-10-175-608-50
; Sequence 50, Application US/10175608
; Publication No. US20040181044A1
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OK APPLICATION UNMERS: 09/635,249
FILING DATE: 07-AUG-2000
PILING DATE: 07-AUG-2000
PPLICATION NUMERS: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,255
FILING DATE: 25-NOV-1992
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 98.5
Matches 270; Conservative
                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-224-683-50
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98.9%; Score 1381; DB 4; Length 27;
Best Local Similarity 98.9%; Pred. No. 2.7e-120;
Matches 270; Conservative 0; Mismatches 3; Indels
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELEPHONE: 312/474-0448
TELEPHONE: 312/474-0448
TELEPHONE: 312/474-0448
TELEPHONE: 312/474-0468
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-175-608-50
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Sequence Seq

5524, 528, 5330, 5331, 534, 503, 503, 511, 511, 511,

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STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUTRY: United States of America COMPUTER: ENDOS SOSTWARS: Patentin Release #1.0, Version #1.30 CORPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARS: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/353,783 FILING DATE: 24-MAY-1995 APPLICATION NUMBER: 08/172,329 FILING DATE: 21-DE-1993 APPLICATION NUMBER: 07/684,535 FILING DATE: 25-NOV-1992 APPLICATION NUMBER: 07/589,701 FILING DATE: 01-OCT-1990 APPLICATION NUMBER: 07/573,616 FILING DATE: 11-JUN-1990 APPLICATION NUMBER: 07/573,198 FILING DATE: 11-JUN-1990 APPLICATION NUMBER: 07/573,198 FILING DATE: 11-JUN-1990 APPLICATION NUMBER: 07/422,383 FILING DATE: 11-JUN-1990 APPLICATION NUMBER: 07/422,383 APPLICATION NUMBER: 07/422,383
US-11-176-830-512
US-11-176-830-514
US-11-176-830-528
US-11-176-830-524
US-11-176-830-524
US-11-176-830-531
US-11-176-830-531
US-11-176-830-531
US-11-176-830-532
US-11-176-830-542
US-11-176-830-542
US-11-176-830-507
US-11-176-830-511
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NAME: Clough, David W . .
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
       ccccccccccccccccccc
       ; Search time 10.5289 Seconds (without alignments) 386.005 Million cell updates/sec
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1 MKKTQTWILTCIYLQLLLFN.....NBEDNBISMLQEKEREFQEV
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1: /cgnZ 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgnZ -6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
3: /cgnZ 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*
4: /cgnZ 6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
5: /cgnZ 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
6: /cgnZ 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
7: /cgnZ 6/ptodata/2/pubpaa/USO10NEW PUB.pep:*
8: /cgnZ 6/ptodata/2/pubpaa/USO10NEW PUB.pep:*
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Biocceleration Ltd.
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US-10-353-783-61
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US-10-519-390-24
US-11-176-830-520
US-11-176-830-529
US-11-176-830-529
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
                                                                                                                    protein search, using
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Minimum DB Maximum DB

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Title: Perfect score:

Sequence:

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Scoring table:

Result

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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-353-783-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, Application US/10353783; Publication No. US20050261175A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                TELEX: «Unknown»
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                        TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-353-783-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                           MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                        Gaps
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1. Sequence 61, Application US/10353783
1. Publication No. US20050261175A1
1. GENERAL INFORMATION:
1. Sugge, Sidney V.
1. Sugge, Sidney V.
1. Martin, Francis H.
1. TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
1. CORMESSONDENCE ADDRESS:
2. ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6310 Sears Tower, 233 South Wacker Drive CITY: Chicago
2. STREET: 6310 Sears Tower, 233 South Wacker Drive COMPTR: United States of America
2. COMPTR: United States of America
3. STATE: 111inois
3. COMPUTER: IB PC Compatible
3. COMPUTER: IB PC Compatible
3. COMPUTER: IP PC Compatible
4. COMPUTER: IP PC Compatible
5. COMPUTER: Patentin Release #1.0, Version #1.30
6. CURRENT APPLICATION NUMBER: US/10/353,783
7. FILING DATE: 28-030-2003
7. FILING DATE: 28-04-2003
7. FILING DATE: 21-DE-1992
7. FILING DATE: 21-DE-1992
7. FILING DATE: 21-DE-1992
7. FILING DATE: 25-NOV-1992
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                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1397; DB 6; Length 273; Best Local Similarity 100.0%; Pred. No. 8.2e-118; Matches 273; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
JOPOLCGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-353-783-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                             INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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US-10-353-783-61
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 KPFWLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAWALPALFSLIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISBGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
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APPLICANT Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Childrogo
STATE: 11linois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
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APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/517,198
FILING DATE: 11-UNM-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-COT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1397; DB 6; Best Local Similarity 100.0%; Pred. No. 8.2e-118; Matches 273; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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KOLKKSPKSPEPRLFTPERPFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKOSRVSVT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MDVLPSHCWISEMYVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVBCVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPFMLPPVAASSLRNDSSSSNRKAKNPTGDSSLHWAAMALPAFFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQILLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 273;
                                                                                                               CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
CONPUTER: Isopoy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ison PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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98.9%; Pred. No. 2.2e-116;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-ANG-1990
APPLICATION NUMBER: 07/573,616
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.9
Matches 270; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWPAMALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.6%; Score 1392; DB 6;
99.6%; Pred. No. 2.3e-117;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
                                                                                                                                 APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
FILING DATE: 24-MAY-1995
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-MOV-1992
APPLICATION NUMBER: 07/684,335
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 50, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                        FILING DATE: 28-Jan-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-10-353-783-50
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SCHEALL INFOGRATION:
SCHEAL INFOGRATION:
SCHEAL INFOGRATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Ustranti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc;
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/467,135
FRIOR PILING DATE: 2002-09-09
FRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SEQ ID NO 520
LENGTH: 248
FUND THE TABLE TAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSFKSPEPRLFTPREFFRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 RSIDAFKOFVVASETSDCVVSSTLSPEKOSRVSVTKPFWLPPVAASSLRNDSSSSNRKAK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 NPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 EGICRARVTANVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.6%; Score 1265; DB 7; L
Best Local Similarity 100.0%; Pred. No. 4.7e-106;
Matches 248; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 10/658, 834
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2002-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA85450
DATABASE ENTRY DATE: 1996-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 520, Application US/11176830; Publication No. US20060020116A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-176-830-520
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       LENGTH: 248
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Best Local {
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APPLICANT: MEDEXGEN Inc.
APPLICANT: CHUNG, Yong-Hoon
APPLICANT: CHUNG, Yong-Hoon
APPLICANT: ILEE, Hak-sup
APPLICANT: ILEE, Hak-sup
APPLICANT: KIM, Jae-Youn
APPLICANT: HEO, Youn-Hoo
TITLE OF INVENTION: A method of improving efficacy of biological response-modifying
TITLE OF INVENTION: proteins and the example muteins
FILE REFERENCE: 2004-12-23
CURRENT APPLICATION NUMBER: KR10-2003-0051846
PRIOR PRILING DATE: 2003-07-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Kopatentin 1.71
SEQ ID NO 24
LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z
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Sequence 206, Application US/11176830

Sequence 206, Application US/11176830

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Guyon, Thierry

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Partice OF INVENTION: Acid Molecules and Related Applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: SCF: 63rd, 102nd, 110th, 115th, 116th, 119th, 126th, 129th, corner in replaced by Val. US-10-519-390-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
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                                               241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
      241 OPSITRAVENIQINEEDNEISMLOEKEREFOEV
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                                                                                                                                                                                                                                          Sequence 24, Application US/10519390
Publication No. US20060008872A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 17109-012002
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Matches 248; Conservative
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KEREFOEV 248
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Sequence 519, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Lila

APPLICANT: Gantier, Lila

APPLICANT: OFFICANT: Diffication of Cytokines for Higher Stability, Encoding in TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: DATE: 2005-07-06

PRIOR APPLICATION NUMBER: 10/558,834

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR APPLICATION NUMBER: 60/409,898

PRIOR PILING DATE: 2002-09-09

SEQ ID NOS: 1306

SOFTWARE: PSEASEQ for Windows Version 4.0

SEQ ID NO 519

LENGTH: 248

TURNER TO SEQ ID NOS: 1306
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Publication No. US20060020116A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gayon, Thierry
APPLICANT: Grantier, Lila
APPLICANT: Uses, Manuel
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION NUMBER: US/11/16,830
CURRENT FILING DATE: 2005-07-06
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
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Best Local Similarity 99.6%; Pred. No. 8.6e-106;
Matches 247; Conservative 1; Mismatches 0;
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CORGANISM: Homo sapiens
US-11-176-830-519
  241 KEREFOEV 248
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| Sequence 537, Application WS/11176830
| Publication No. US20060020116A1
| GENERAL INFORMATION:
| APPLICANT: Gantier: Rene
| APPLICANT: Usery
| APPLICANTON NUMBER: US/1/176,830
| CURRENT APPLICATION NUMBER: US/458,834
| PRIOR PILING DATE: 2003-09-08
| PRIOR PPLING DATE: 2003-09-08
| PRIOR PPLING DATE: 2003-09-09
| NUMBER OF SEQ ID NOS: 1306
| SEQ ID NO 537
| LENGTH: 248
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                                                                                                                          86 DKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSPKSPEPRLFTPBEFFRIFN 145
                                                                                                                                                                                                                   146 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAASSLRNDSSSSNRKAK 205
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                                        26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
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  0; Gaps
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  0; Indels
1; Mismatches
247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-537
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Best Local S:
Matches 247,
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APPLICANT: Gantier, Rene

APPLICANT: Gantier, Rene

APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: User, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
FILE REFERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2002-09-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 538
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202
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; Sequence 499, Application US/11176830
; Publication No. US20060020116A1
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Matches 247; Conservative
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Sequence 536, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gauyon, Thierry

APPLICANT: Gayon, Thierry

APPLICANT: Gayon, Thierry

APPLICANT: Use, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION NUMBER: US/11/176,830

CURRENT APPLICATION NUMBER: US/68,834

PRIOR PLILING DATE: 2003-09-08

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR PRILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 536

LENGTH: 248
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99.6%; Pred. No. 8.6e-106;
tive 1; Mismatches 0;
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90.3%; Score 1262; DB 7;
Best Local Similarity 99.6%; Pred. No. 8.6e-106;
Matches 247; Conservative 1; Mismatches 0;
  PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 529
LENGTH: 248
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Best Local Similarity 99.6
Matches 247; Conservative
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US-11-176-830-536
                                                                                                                                                        , ORGANISM: Homo sapiens
US-11-176-830-529
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US-11-176-830-536
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GENERAL INFORMATION

APPLICANT: Gautier, Rene
APPLICANT: Gautier, Rene
APPLICANT: Gautier, Rene
APPLICANT: Gautier, Lilia
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REPERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2003-09-08
FRIOR FILING DATE: 2003-09-08
FRIOR FILING DATE: 2003-09-08
FRIOR FILING DATE: 2003-09-09
FRIOR FILING DATE: 2003
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                                                                                                                                                           Query Match 90.3%; Score 1261; DB 7;
Best Local Similarity 99.6%; Pred. No. 1.1e-105;
Matches 247; Conservative 1; Mismatches 0;
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Best Local Similarity 99.6%; Pred. No. 1.1e-105;
Matches 247; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 501, Application US/11176830 Publication No. US20060020116A1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-500
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US-11-176-830-501
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            APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Oritanti, Lila
APPLICANT: Vega, Manuel
TITLB OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 1109-01202 (9228)
CURRENT APPLICATION NUMBER: 10/658,834
PRIOR APPLICATION NUMBER: 10/658,834
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 499
LENGTH: 248
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90.3%; Score 1261; DB 7;
Best Local Similarity 99.6%; Pred. No. 1.1e-105;
Matches 247; Conservative 1; Mismatches 0;
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US-11-176-830-499
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266 KEREFQEV 273 |||||||| 241 KEREFQEV 248

Search completed: February 22, 2006, 18:27:28 Job time : 10.5289 secs

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Scoring table:

Searched:

Database

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New naturally-occurring polypeptide stem cell factor analogues - have haematopoietic biological activity of stem cell factor and are used to treat e.g. leukopenia, AIDS, nerve damage and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Stem Cell Factor from 5637 bladder carcinoma line.
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                          AAB96941
AAB93567
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/label=_sig-peptide
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90US-00537198.
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90WO-US005548.
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Zsebo KM, Suggs SV,
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N-PSDB; AAQ11543.
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11-JUN-1990;
24-AUG-1990;
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01-OCT-1990;
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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genescqp2001s:
genescqp2003as:
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genescqp2003bs:
genescqp2004s:
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Maximum DB seq length: 200000000
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The SCF has the ability to stimulate growth of primitive progenitors including early hematopoietic progenitor cells and non- hematopoietic

Disclosure; Fig 44; 127pp; English.

Human Human

Human Human

AAY53284 AAB98367 AAB98357

Result No.

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BFQEV 245
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N-PSDB; AAT04891
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germ stem cells. The
stem cells such as neural stem cells and primordial germ stem cells. The product may be used in a pharmaceutical compsn. for treating, in a mammal, leukopenia, thrombocytopenia, anaemia, AIDS, neoplasia, nerve damage, infertility and intestinal damage. See also AAR11/08, AAQ11509-
                                                                                                                      1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Stem cell factor; progenitor; haematopoiesis; SCF; anaemia; thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft; transplant; neoplasia; myelosuppression; bone marrow; ss.
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                                                                        Length 245;
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ive 0; Mismatches 0
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                                                       Sequence 245 AA;
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28-SEP-1990;
01-OCT-1990;
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15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1990;
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carcinoma cell line. Non-naturally occuring SCF and C-terminally carcinoma cell line. Non-naturally occuring SCF and C-terminally curroated polypeptides, having amino acid sequences sufficiently compared to naturally occuring SCF stimulate growth of printitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition of contracting leucopenia, anaemia or thrombocytoponia, for enhancing engrathment of bone marrow during transplantation or for bone marrow aplasia or recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertlilty, intestinal damage or myelosupointerion or for bone may be raised against the peptides for use in detection or hibbodies may be raised against the peptides for use in detection or antibodies may be raised against the peptides for use in detection or and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                              AAR83979 is a human stem cell factor (SCF) derived from the 5637 bladder
New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood
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                                                                                                                                                            Claim 9; Fig 44; 127pp; English.
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The present sequence representing human SCF (stem cell factor) protein is isolated from the 5637 bladder carcinoma cell line. The present invention crlates to novel stem cell factors (AA002453-AA002466) and the polymucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AA00462-AA002481) and the oligonucleotides (AA0040117) used in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in CC apen therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hoddkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, congestive splenomegaly, pyridoxine deficiency, and hypopigmentation cand folic acid deficiency, pyridoxine deficiency, and hypopigmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
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 blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder; 5637 bladder carcinoma.
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100.0%; Pred. No. 3e-121;
tive 0; Mismatches 0
                                                                                                                       Example 5; Fig 44A-44C; 209pp; English.
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                                                                                                                 Location/Qualifiers
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/label= Mature_SCF
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90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
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Matches 245; Conservative
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SUGGS S V.
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01-OCT-1990;
21-DEC-1993;
                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for enhancing (B) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCP) receptor to a biologically active SCP, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. Addition to Addition of the present AAB98390 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                     Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide
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Pred. No. 3e-121;
                                                                                                                                                                                                             Suggs SV, Martin FH;
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100.0%; Pred. No. score
0; Mismatches
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89US-00422383.
90US-00537199.
90US-00573616.
92US-00982255.
93US-00172322.
95US-00449653.
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           GDSSLHWAANALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, sarcoidosis.
                                                                                                                                                                                                                                      Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1262; DB 4;
Pred. No. 3e-121;
                                                                                                                                                                                                                                                                                                                                        1. .25
/label= signal_peptide
26 . .245
/label= mature_stem_cell_factor
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                                                                                                                                                                                                                    Human stem cell factor SEQ ID NO: 63.
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                                                                                                                                              AAB96953 standard; protein; 245 AA
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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                                                                                                                                                                                             (first entry)
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N-PSDB; AAF89105.
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Best Local Similarity
                                                                                  EFOEV 245
                                                            EFQEV 245
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
                                                                                                                                           61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                           1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLFKDYMITLKYVPG
                                               MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                               KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKGKAKNPP
 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                           Human, stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                  Human SCF protein isolated from the 5637 bladder carcinoma cell line
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/label= Signal_peptide
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/label= Mature_SCF
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
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                                                                                                                                                                                                                                                                                                                                                                                                                  5637 bladder carcinoma.
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
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isolated from the 5637 bladder carcinoma cell line. The present invention relates to novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the polymucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides (AAH23895) used in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Rodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicaemia, malaria, vitamin hypopigmentation disorders such as piebaldism and vitiligo
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                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, stem cell factor; SCF, early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SCF protein isolated from the 5637 bladder carcinoma cell line.
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                                                                                                                                                                                                            Query Match 100.0%; Score 1262; DB 4; Length 245; Best Local Similarity 100.0%; Pred. No. 3e-121; Matches 245; Conservative 0; Mismatches 0; Indels 0;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            BFQEV 245
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                                                                                                                                                                                        Sequence 245 AA;
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11-JUN-1990;
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121 KOLKKSFKSPEPRLFTPEEFRIFNRSIDAFKOPVASSALLE
121 KOLKKSFKSPEPRLFILIGFAPGALYWKKRQPSLTRAVENIOINBEDNEISMLOEKER 240
181 GDSSLHWAAMALPALFSLIIGFAPGALYWKKRQPSLTRAVENIOINBEDNEISMLOEKER 240
181 GDSSLHWAAMALPALFSLIIGFAPGALYWKKRQPSLTRAVENIOINBEDNEISMLOEKER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence representing human SCF (stem cell factor) protein is isolated from the 5637 bladder carcinoma cell line. The present invention relates to novel stem cell factors (AAU02761-AAU02775, AAU02779, AAU02797) and the polymuclectides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF speptides (AAU027794) and the coligonuclectides (AAS04182-AAS0418) used in the isolation of human and rat SCF sequences. The polymuclectide encoding SCF is useful for treating carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, archinoma, daucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcidosis, military tuberculosis, disease, carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, sarcidosis, military tuberculosis, disease, carcidosis, military tuberculosis, disease, carcidosis, military tuberculosis, disease, chiminating septicemia, malaria, vitamin Blz and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early hematopoietic progenitor cells.
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                                                                                                                                                                                                                                         Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 44A-44C; 167pp; English
                                                                                                                                                                                                                                             Suggs SV,
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90US-00573616.
90US-00589701.
92US-00982255.
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                                                                                                                                                          (AMGE-) AMGEN INC.
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The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally-occurring SCF to allow possession of haematopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemotherapeutic induced home marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, nooplasia, infertility, myeloproliferative disorder, intestinal damage in a mammal. SCF sequences are useful for preparing blologically active polymer polypeptide adduct, for enhancing transfection of early
181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
                                                                                                                                                                                                                                                                                                                                                                                    Human; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myelostoliferative disorder; infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; hedgkin; s disease; lymphoma; Gaucher's disease; Niemann-Pick disease; Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia; disseminated fungus disease; Pulminating septicaemia; piebaldism; AIDS; acquired immune deficiency syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitamin Bl2 deficiency; folic acid deficiency; blamond Blackfan anaemia; hypopigmentation disorder; vitiligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
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    .25
    /label= Signal_peptide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                        AAE22327 standard; protein; 245 AA.
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(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                Human SCF protein #3
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                                               241 EPQEV 245
                                                                                        EPQEV 245
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                                                                                                                                                                                                                                                      AAE22327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
                                                                                          1. .25
/label= Signal_peptide
26. .245
/label= Mature_SCF
                                                                     Location/Qualifiers
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900S-00573616.
900S-00589701.
910S-00684535.
920S-00982255.
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(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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                          Homo sapiens
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25-NOV-1992;
21-DEC-1993;
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01-OCT-1990;
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RESULT 11
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haematopoietic progenitor cells with a gene, and transfer of a gene into a mammal. They are useful for treating myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Sive disease, refractory erythroblastic anaemia, Di Guglielmo syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary splenic pancyropaenia, disseminated fungus disease, malaria, military tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin Bl2 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation disorders such as piebaldism, AIDS (acquired immune deficiency syndrome) and vitiligo. The present sequence is human SCF protein
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90US-00537198.
90US-00573616.
90WS-US005548.
90EP-00310899.
95EP-00105391.
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                                                                                                                                                                                                                                                                     Sequence 245 AA;
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11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
04-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel stem cell factors (SCFB), polynucleotide sequences encoding the SCFB, and methods of producing them. SCFB are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCP. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence represents human SCF protein isolated from the 5637 bladder carcinoma cell line
                                                                                                                                                                                            Production of a human stem cell factor (SCP) polypeptide for treating disorders involving blood cells, such as leukemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                       Martin
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                                                       Bosselman RA,
                                                                                                                                                                                                                                                                                                                                          Example 18; Fig 44; 120pp; English.
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                                                                                                                                                                                                                                                                                       encoding the human SCF
                                                     Suggs SV,
                                                                                                          WPI; 2002-684093/74.
N-PSDB; ABS73860.
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(AMGE-) AMGEN INC.
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                                                       Zsebo KM,
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120 120 180 180

ADP99333;

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ADP99333 standard; protein; 245 AA
ADP99333
             The invention relates to stem cell factor (SCF) polypeptides with haematopoietic activity and the polymucleotides encoding them. The polypeptides are used for treating infertility, intestinal damage, myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of improving engraftment of bone marrow transplants, for enhancing bone arcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF polypeptides and also as probes for mapping of the SCF gene, for polypeptides and also as probes for mapping of the SCF gene, for identifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents an SCF polypeptide of the
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                                                                                                                                                                                                                                                                                                                                  New non-natural stem cell factor, useful for treating e.g. leucopenia or immune deficiency, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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                                                                                                                                                                                                                                                             Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                               Claim 9; SEQ ID NO 63; 217pp; English
                                                    9005-00537198.
9005-00537198.
9005-00589701.
9105-00684535.
9205-00982255.
9305-00172329.
9505-0017329.
            98US-00224683
                                        89US-00422383
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Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                              Zsebo KM, Bosselman RA,
                                                                                                                                                                                      (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                          WPI; 2003-851459/79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 245 AA;
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             31-DEC-1998;
                                                                      24-AUG-1990;
01-OCT-1990;
                                                                                                   10-APR-1991
25-NOV-1992
                                                                                                                                                         12-JAN-1998
                                                         11-JUN-1990
                                                                                                                              21-DEC-1993
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12

RESULT

셤 ઠે 셤 δ 원 ઠ 셤 ò

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Human, SCF; stem cell factor; gene therapy;

Maematopoietic progenitor cell; aplastic anaemia;

Maematopoietic progenitor cell; aplastic anaemia;

Macroyermal nocturnal haemoglobinuria; myelofibrosis;

Myelopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma;

Myelopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma;

Myelopetrosis; miltiple; disease; lymphoma; Gaucher's disease; Niemann-Pick disease;

Myelopetrosis; congestive splenomegaly; Kala awar; sarcoidosis;

Myelopetrosis; miltiary tuberculosis;

Myeseminated fungus disease; Pulminating septicaemia; malaria;

Wyitamin Bl2 deficiency; folic acid deficiency; pyridoxine deficiency;

Wyitaligo; neurological damage; infertility; intestinal damage;

Wyelligo; neurological damage; infertility; intestinal damage;

Wyelligo; neurological cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing a human stem cell factor (SCF) polypeptide, useful for treating hematopoletic disorders, e.g., aplastic anemia, comprises growing host cells transformed or transfected with DNA encoding a human SCF.
                                                                Human stem cell factor, SCF, protein (bladder cancer).
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    .25
    /note= "Signal peptide"

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/note= "Mature SCF"
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90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
92US-00172329.
95US-00149182.
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23-SEP-2004 (first entry)
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24-AUG-1990;
01-OCT-1990;
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24-MAY-1995;
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25-NOV-1992
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cc variety of recombinant techniques or for generating new and useful viral and circular plasmid DNA vectors, new and useful transformed and circular plasmid DNA vectors, new and useful transformed and transfected prokaryotic and eukaryotic host cells, and new and useful comethods for cultured growth of such host cells capable of expression of SCF and its related products. The DNA sequences are also useful as a protein synthesis, in genetic therapy in humans and other mammals, and cometin synthesis, in genetic therapy in humans and other mammals, and in developing transgenic mammalian species which may serve as eukaryotic in developing transgenic mammalian species which may serve as eukaryotic consetul for treating haematopoietic disorders, e.g., aplastic anaemia, consetul for treating haematopoietic disorders, e.g., aplastic anaemia, consecutions metastatic carcinoma, acute leukaemia, multiple myeloma, conterer-siwe disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Siwe disease, refractory erythroblastic anaemia, pick disease, congestive splenomegaly, Kala awar, sarcoidosis, primary splenic pancytopaenia, miliary tuberculosis, disseminated fungus disease, Congestive splenomegaly, Kala awar, sarcoidosis, primary splenic pancytopaenia, miliary tuberculosis, disseminated fungus disease, Confidence such as piebaldiam and vitiligo. The SCF are also useful for treating neurological damage, infertility states, intestinal damage cresulting from irradiation or chemotherapy, and AIDS. SCF is also descret sequence is a human SCF protein sequence (partial or full length).

Seguence 245 AA;

ö MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 9 MKKTQT#ILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKOYMITLKYVPG MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAPKOFVVASETSDCVVSSTLSPEKGKAKNPP GDSSLHWAAMALPALFSLIIGFAFGALYWKKROPSLTRAVENIQINEEDNEISMLOEKER 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSOCVVSSTLSPEKGKAKNPP GDSSLHWAAMALPALFSLIIGPAFGALYWKKRQPSLTRAVENIQINBEDNEISMLQEKER ; 0 100.0%; Score 1262; DB 8; Length 245; 100.0%; Pred. No. 3e-121; ive 0; Mismatches 0; Indels 0 Best Local Similarity 100. Matches 245; Conservative EFQEV 245 EPOEV 245 Query Match 61 61 121 121 181 181 241 a ò . 연 g 셤 ò Š ઠે

ADS88051 standard; protein; 245 AA (first entry) 18-NOV-2004 ADS88051; RESULT 13

Tumour treatment-related human protein sequence SeqID87.

240

240

180

120

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tumour inhibition, tumour treatment; metastasis; infectious lesion; antigen presenting cell; immunostimulatory cytokine; cytostatic; vulnerary; immunomdulator; melanoma; hepatoma; adenocarcinoma; colorectal cancer; based cell cancer; oral cancer; nasopharyngeal cancer; laryngeal cancer; badder cancer; head cancer; neck cancer; neck cancer; renal cell cancer; pancreatic cancer; pulmonary cancer; cervical cancer; ovarian cancer; oseophageal cancer; gulmonary cancer; cervical cancer; testicular cancer; breast cancer; human.

ADU50663 standard; protein; 245 AA.

EPOEV

13-JAN-2005 (first entry)

Homo sapiens

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This invention relates to a novel method of inhibiting or treating a tumour, metastasis or infectious lesion in a subject which comprises administrating into or near a site of a tumour or infectious lesion in a subject an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine. The invention may be useful for the production of compounds with a cytostatic or vulnerary activity acting as timunomodulators. The method is useful in inhibiting or treating as timunomodulators. The method is useful in inhibiting or treating a cumour, metastasis or infectious lesion in a subject, where the size of the tumour, metastasis (where number is also decreased) or infectious certing is selected from metanoma, hepatoma, adenocarcinoma, colorectal cancer, basal cell cancer, read and neck cancer, renal cell cancer, pancreatic cancer, pulmonary cancer, cervical cancer, ovarian cancer and breast cancer, gastric cancer, prostrate.
                                                                                                                                                                                                                                                                                                       Inhibiting or treating a tumor, metastasis or infectious lesion comprises administering into or near site of a tumor or infectious lesion an antigen presenting cell and an immunostimulatory cytokine or a nucleic acid encoding the cytokine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKRNSS
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                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 87; 169pp; English
                                                                              15-OCT-2003; 2003WO-US032827
                                                                                                                  15-OCT-2002; 2002US-0418865P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sest Local Similarity 100.
                                                                                                                                                             (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                        Lotze MT, Tahara H;
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WO2004034995-A2
                                        29-APR-2004.
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The invention relates to a stem cell factor (SCP) such as non-naturally-
cocurring SCF having an amino acid sequence sufficiently duplicative of
that of naturally occurring SCF to allow possession of a haematopoietic
biological activity of naturally occurring stem cell factor, or naturally
cocurring SCF. Also included are an isolated DNA sequence for use in
securing SCF. Also included are an isolated DNA sequence for use in
securing SCF. Also included are an isolated DNA sequence for use in
caturally occurring SCF, a prokaryotic nost cell of non-
certansformed or transfected with the DNA, a polypeptide product of the
cxpression of the DNA in a prokaryotic or eukaryotic host cell, an
cypression of non-naturally occurring SCF, a DNA sequence coding for a
polypeptide fragment or polypeptide analogue of naturally-occurring stem
ccell factor, a biologically functional plasmid or viral DNA vector
including the DNA sequence above, a prokaryotic or eukaryotic host cell
citably transformed or transfected with the DNA, a polypeptide having part
cor all of amino acid sequence encoded by composite nucleic acid sequence
cof human SCF cDNA sequence obtained from HT1080
cfibrosarcoma cell line, or human SCF cDNA sequence obtained from 537 bladder
carcinoma cell line (and having one or more of in vitro biological
carcinoma cell line, or human SCF cDNA obtained from an antibody
specifically binding SCF. SCF. is useful for traating leukopaenia,
chrombocytopaenia, anaemia, and enhancing engraftment of bone marrow
during transplantation in a mammal. SCF is useful enhancing bone marrow
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                                                      Human, stem cell factor; SCF; haematopoietic;
HT1080 fibrosarcoma cell line; 5637 bladder carcinoma cell line;
leukopaenia; Hrombocytopaenia; anaemia; bone marrow during transplant;
bone marrow aplasia; myelosupression; immune deficiency; neoplasm;
nerve damage; infertility; intestinal damage;
                                                                                                                                                              myeloproliferative disorder; early haematopoietic progenitor cell; haematopoietic disorders; aplastic anaemia; myelosois; myelosies; myelosoierspetrosis; metastatic carcinoma; multiple myeloma; Hodgkin's disease; lymphoma; gaucher's disease; Niemann-Pick disease; blamond-Blackfan anaemia; DBA; Fanconi's anaemia; gene therapy;
                 Human SCF cDNA from 5637 bladder carcinoma cell line, protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-00537198.
90US-00573616.
90US-00589701.
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92US-00982255.
93US-00172329.
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(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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                                                                                                                                                                                                                                                                          acute blood loss.
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                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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25-NOV-1992
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bone marrow aplasia or myelosuppression which involves treating patients with therapeutically effective doses of SCF. SCF is useful for treating caquired immune deficiency, neoplasia, nerve damage, infertility, intestinal damage, and a myeloproliferative disorder. SCF is useful for treating carly haematopoletic progenitor cells with a gene which cransfecting early haematopoletic progenitor cells with SCF, and transfecting the cultured cells with a gene which cransfecting a gene to a mammal which involves culturing early cransfecting a gene to a mammal which involves culturing early cransfecting the cultured cells with a gene, and administering the cultured cell to the mammal. SCF is useful for treating various haematopoletic disorders, aplastic anaemia, complicible myelomia haematopoletic disorders, aplastic anaemia, myelofibrosis, myelomia haematopoletic disorders, aplastic anaemia, multiple myeloma, hodgkin's disease, lymphoma, gaucher's canaemia. SCF is useful for enhancing the efficiency of gene therapy, for enhancing haematopoletic recovery after acute blood loss. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1262; DB 8; Length 245; 100.0%; Pred. No. 3e-121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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    .25
    label= Signal_peptide

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/label= Mature protein
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 245; Conservative (
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The present invention relates to a method (MI) for stimulating proliferation of melanocyte cells in a human. (MI) involves administering CC proliferation of melanocyte cells in a human. (MI) involves administering CC that stimulates growth of melanocyte cells, and optionally a carrier, to the thuman. The SCF is covalently conjugated to a water soluble polymer CC e.g. polyethylene glycol. Also, the SCF is co-administered with one or more other cytokines. SCF is also able to stimulate the growth of printitive progenitors such as early hematopoietic progenitor cells that are capable of maturing to erythroid, megakaryccyte, granulocyte, come macrophage cells, and non-hematopoietic stem cells such as collerating bone marrow regeneration, and in augmenting T cell accelerating bone marrow regeneration, and in augmenting T cell production. (MI) is useful for treating stem cells disorders that are characterized by a reduction in functional marrow mass due to toxic, radiant or immunological injury. (MI) is useful in treating AIDS, confluction in functional marrow mass due to toxic, radiant or immunological injury. (MI) is useful in treating AIDS, well-intended proposition of disease, lymphoma, Gaucher's disease, Niemann Prick disease, congestive splenomegaly, Kalaazar, sarcoidosis, primary splenic pancytopenia, vitamin B12 and folic acid deficiency disease, pyridoxine deficiency disease, and hypopigmentation disorders such as confluence resulting from irradiation or chemotherapy, and stem cell myeloproliferative disorders such as chronic myelogenous leukemia, primary thromboocythemia and acute leukemia. (MI) is useful in expanding call myeloproliferative disorders such as chronic myelogones contranglantation, and in enhancing the efficacy of gene therapy. The present sequence was used to illustrate the invention. The call therapy the present sequence was used to illustrate the invention. The call was accompanied to the cape of the cape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stimulating proliferation of melanocyte cells in human, involves administering stem cell factor polypeptide or its biologically active fragments stimulating growth of melanocyte cells, and optionally carrier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequence for this protein was obtained from the 5637 bladder carcinoma cell line.
                                                                                                                                                                                                                                                                                                                                                                   Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 63; 212pp; English
                                                                                                                                                                                                                                                                                                                                                                   Sugge SV,
                                                                                                                       89US-00422383.
90US-00537198.
90US-00573616.
91US-00689701.
91US-00684535.
93US-00982255.
                                                                                  2000US-00604325
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                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADW93107
                                                                                  26-JUN-2000;
  US6852313-B1
                                                                                                                                                                                                                                                                              24-MAY-1995;
                                       08-FEB-2005
                                                                                                                            16-OCT-1989
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01-OCT-1990
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0; Gaps

Query Match 100.0%; Score 1262; DB 9; Length 245; Best Local Similarity 100.0%; Pred. No. 3e-121; Matches 245; Conservative 0; Mismatches 0; Indels 0

MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120

61

6 8 8

240 240 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120 121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKGKAKNPP 181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINBEDNEISMLQBKER GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER KDLKKSFKSPEPRLFTPEEFFRI FNRSI DAFKDFVVASETSDCVVSSTLSPEKGKAKNPP **EFQEV 245 BFOEV 245** 181 241 241 121 셤 Ś 셤 Š 셤 ò

Search completed: February 22, 2006, 18:13:01 Job time : 145.098 secs

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us-10-620-642-63.rpr

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 22, 2006, 18:13:23 ; Search time 20.2479 Seconds (without alignments) 1164.223 Million cell updates/sec Run on:

US-10-620-642-63 1262 1 MKKTQTWILTCIYLQLLLFN......NBEDNEISMLQBKERBFQEV 245 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mast cell growth f	mast cell growth f	c-kit ligand - pig	mast cell growth f	stem cell factor,		mast cell growth f			_	_	_			mast cell growth f	probable advanced	transcription init	hypothetical prote	conserved hypothet	probable ubiquitin	citrate (pro-3S)-1	hypothetical prote	cal	secz	helicase (EC 3.6.1	hypothetical prote	lactose transport	sodium channel SCA	formate dehydrogen
SUMMARIES	ΩΙ	B61190	A35974	146575	A37934	847571	146929	865801	S58313	B35974	S70367	JN0637	S70366	\$29052	B35971	A35971	T09062	537845	F82909	F90595	T37964	G86773	T23425	E90553	AD1507	ндвхрн	AC2939	D98343	T30902	F64300
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	Length	245	273	274	245	274	274	273	202	201	253	287	287	124	51	49	402	482	1447	647	3227	512	534	420	821	1174	295	309	1993	378
	Query Match	100.0	97.5	82.2	81.0	80.7	80.4	78.5	59.4	57.1	47.9	46.3	46.2	38.9	13.9	13.7	7.7	7.7	7.7	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.2
	Score	1262	1231	1037.5	1022	1018.5	1014.5	166	749.5	721	605	584	583	491.5	175.5	172.5	97.5	97	97	93.5	93.5	92.5	92.5	92	92	92	91.5	91.5	91.5	91
	Result No.	п	8	n	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

241 EPQEV 245

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ATP-dependent Clp	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	genome polyprotein	phosphoenolpyruvat	hypothetical prote	replication initia	hypothetical prote	hypothetical prote	phosphoenolpyruvat	hypothetical prote	hypothetical prote	hypothetical prote
A69136	S70770	C86613	B72012	T26656	RRVUBY	H84855	F71856	S74840	T19850	S51404	S26235	T27886	T19295	T22794
01 0	v 0	~	~	~	Н	N	N	7	N	~	~	~	7	7
616	1675	411	411	1384	2238	941	1154	447	246	570	996	1293	1813	099
7.2	7.7	7.1	7.1	7.1	7.1	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9
90.5	90.5	90	90	89	89	88.5	88.5	88	87.5	87.5	87.5	87.5	87.5	87
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 198; Conservative
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A,Status: prelimina
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146575

c-kit ligand - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (acceptance_revision 21-Reb-1997 #text_change 09-Jul-2004

C;Accession: 146575

R;Zhang, Z.; Anthony, R.V.

Biol. Reprod. 50, 95-102, 1994

A;Title: Porcine stem cell factor/c-kit ligand: its molecular cloning and localization

A;Reference number: 146575; MUID:94146218; PMID:7508758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
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Pred. No. 1.7e-91;
0; Mismatches 1; Indels 2
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Best Local Similarity 89.4%;
Matches 244; Conservative
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A;Molecule type: mRNA
*Residues: 1-274 «ZHA»
A;Cross-references: UNIPROT:Q29030; UNIPARC:UPI0000135640; GB:L07786; NID:g164420; PIDN:
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NyAlternate names: KL-2 protein
NyAlternate names: KL-2 protein
CiSpecies: Mus musculus (house mouse)
CjSpecies: Mus musculus (house mouse)
CjAcession: A37934; B43751
CjAcession: A37934; B43751
Cell 64, 1025-1035, 1991
A;Filanagan, J.G.; Chan, D.C.; Leder, P.
Cell 64, 1025-1035, 1991
A;File: Transmembrane form of the kit ligand growth factor is determined by alternative A;Reference number: A37934; MUID:91160046; PMID:1705866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A37934
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mLNA
Cross-references: UNIPROT:P20826; UNIPARC:UPI000002B352; GB:M64262
R;Huang, B.J; Nocka, K.H.; Buck, J.; Besmer, P.
R;Huang, B.J; Nocka, K.H.; Buck, J.; Besmer, P.
A)C. Biol. Cell 3, 349-362, 1992
A;Title: Differential expression and processing of two cell associated forms of the kit-A;Reference number: A43751; MUID:92330001; PMID:1378327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MDVLPSHCWISEMVBQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECMEEHSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TKPFMLPPVAASSLRNDSSSSNRKASDSIEDSSLQWAAVALFAFFSLVIGFAFGALYWKK 240
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                                                                                                                                                                                                                               Gaps
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A;Residues: 1-173,'R',175-186,'L',188-245 <HUA>
A;Cross-references: UNIPARC:UP10000179560; GB:S04534
A;Note: the authors translated the codon TTG for residue 187 as Trp
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                               DB 2; Length 274;
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                                                                                                                                                                                                                            Indels
                                                                                                                                                            Query Match 82.2%; Score 1037.5; DB 2; Best Local Similarity 75.2%; Pred. No. 5.9e-76; Matches 206; Conservative 22; Mismatches 17;
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Matternate names: hematopoietic growth factor KL; ligand steel factor; stem cell factor (Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence revision 27-Feb-1897 #text change 09-Jul-2004
C;Accession. 565801; A43751; A35976; A35972; A35975; A35973; I48768
R;Bedell, M.A.; Copeland, N.G.; Jenkins, N.A.
Genetics 142, 927-934, 1996
A;Title: Multiple pathways for Steel regulation suggested by genomic and sequence analy. A;Reference number: 565801; MUID:97002551; PMID:8849898
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A; Molecule type: mRNA
A; Residues: 1-214, 'L', 216-273 «HUA>
A; Residues: 1-214, 'L', 216-273 «HUA>
A; Cross-references: UNIPARC: UPIO00014D0C1; GB: S40364; NID: 9251668; PIDN: AAB22554.2; PID
A; Note: the authors translated the codon TTG for residue 215 as Trp
R; Huang, E.; Nocka, K.; Beier, ·D.R.; Chu, T.Y.; Buck, J.; Lahm, H.W.; Wellner, D.; Leder Cell 63, 225-233, 1990
A; Title: The hematopoietic growth factor KL is encoded by the Sl locus and is the ligan A; Reference number: A55976; MUD: 91004221; PMID: 1698557
A; Accession: A55976
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A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-206,'S',208-270 <HUZ>
A;Residues: 1-206,'S',208-270 <HUZ>
A;Residues: 1-2076,'S',208-270 <HUZ>
A;Cross-reneces: UNIPARC:UPIO00017955D; GB:M38511
B;Anderson, D.M.; Lyman, S.D.; Baird, A.; Wignall, J.M.; Eisenman, J.; Rauch, C.; March, Cell 63, 235-243, 1990
A;Title: Molecular cloning of mast cell growth factor, a hematopoietin that is active in A;Reference number: A35977; MUID:91004223; PMID:1698558
A;Accession: A35977
A;Accession: A35977
A;Accession: A35977
A;Residues: 1-273 <AND>
A;Residues: 1-273 <AND>
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A;Title: Mast cell growth factor maps near the steel locus on mouse chromosome 10 and ir A;Reference number: A35972; MUID:91004216; PMID:1698554
                                                                                                                                                                                                                                                                                                                                                              61 MDVLPSHCWISVWVBQLSVSLTDLLDKFSNISEGLSNYSIIDKLVKIVDDLVECTEGYSF 120
                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
    9
                                                MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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A;Molecule type: mRNA
A;Residues: 26-53 <COP>
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Cipate: O. dog
Cipate: O. desp-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
Cipate: O. d-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
Cipate: O. d-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
Cipate: O. d-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
Cipate: O. dogs of the control of control of the contro
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;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47571
B;Chou, J.H.; Hikono, H.; Ohtaki, M.; Kubota, T.; Sakurai, M.
B;Chim. Biophys. Acta 1223, 148-150, 1994
A;Title: Cloning and characterization of cDNAs encoding two normal isoforms of bovine 8
A;Accession: S47571
A;A
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                             MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47571
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80.4%; Score.1014.5; DB 2; Length
Best Local Similarity 74.8%; Pred. No. 4.2e-74;
Matches 205; Conservative 17; Mismatches 23; Indels
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A,Residues: 1-202 <MCI>
A,Cross-references: UNIPROT:P79368, UNIPARC:UPI000016C4E5; EMBL:Z50743; NID:G940807; PID
C,Superfamily: mouse mast cell growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 59.4%; Score 749.5; DB 2; Length Best Local Similarity 83.9%; Pred. No. 5.5e-53; Matches 146; Conservative 15; Mismatches 12; Indels
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A; Status: preliminary
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A;Cross-references: UNIDARC:UP1000017955E; GB:MS5912
R;Zeebo, K.M.; Williams, D.A.; Gediseler, E.N.; Broudy, V.C.; Martin, F.H.; Atkins, H.L.; Cattanach, B.M.; Galli, S.J.; Guggs, S.V.
Cattanach, B.M.; Galli, S.J.; Guggs, S.V.
A;Title: Grem cell 16acror is encoded at the S1 locus of the mouse and is the ligand for A;Reference number: A35975; MUD191004220; PMID:1698556
A;Accession: A35975
A;Accession: A35975
A;Accession: A35975
A;Residues: 1-201 - 4258-
A;Residues: 1-201 - 4258-
A;Residues: 1-201 - 4258-
A;Cross-references: UNIPRAKC:UP1000016D02D; GB:MS9915; NID:G200935; PIDN:AA40095.1; PID:
A;Eaebo, K.M.; Wypych, J.; McNiece, I.K.; Luu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev, A.; Langley, K.M.; Wypych, J.; McNiece, I.K.; Luu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev, A.; Langley, K.M.; Wypych, J.; McNiece, I.K.; Luu, H.S.; Smith, K.A.; Karkare, S.B.; Sachdev, A.; Langley, K.M.; Protein and biological characterization of hematopoietic A;Reference number: A35973
A;Accession: A35973
A;Accession: A35973
A;Accession: A;Residues: Drotein
A;Residues: 27-29; R', 11-39 - 4252-
A;Accession: Midney Brotein
A;Residues: Developmental abnormalities in Steelliff mice result from a splicing defect in CA;Reference number: A40717; MUD:93012940; WDBJ
A;Accession: 14976
A;Accession: 14977
A;Accession: 14976
A;Accession: 14976
A;Accession: 14977
A;Accession: 14977
A;Accession: 14976
A;Accession: 14977
A;Accession: 14977
A;Accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KPFMLPPVAASSLRNDSSSNRKAAKAPEDSGLQWTAMALPALISLVIGPAFGALYWKKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDIKKSFKSPEPRLFTPEEFFRIFURSIDAFKDFVVASETSDCVVSSTLSPEKG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.5%; Score 991; DB 2; Length 273; Best Local Similarity 72.2%; Pred. No. 3.2e-72; Matches 197; Conservative 19; Mismatches 29; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
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C;Species: Rattus norregicus (Norway rat)
C;Date: 14-Dec-1990 #text_change 09-Jul-2004
C;Date: 14-Dec-1990 #text_change 09-Jul-2004
C;Date: 14-Dec-1990 #text_change 09-Jul-2004
C;Date: 14-Dec-1990 #text_change 09-Jul-2004
C;Date: 14-Dec-1990 #text_change, C.V.; Mypych, J.; Morris, C.F.
R;Martin, F.H.; Suggs, S.V.; Langley, K.E.; Lu, H.S.; Ting, J.; Okino, K.H.; Morris, C.F.
Call 63, 203-211, 1990
A;Pitle: Primary structure and functional expression of rat and human stem cell factor D
A;Reference number: A35974; MUID:91004219; PMID:2208279
A;Reference number: A35974
A;Reference number: A35974
A;Residue: 1-201 cMAR>
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: MRNA
A;Molecule type: MSNA
A;Molecule type: MSNA
A;Residues: 1-201 cMAR>
A;Residues: 1-201 cMAR>
A;Residues: 1-201 cMAR>
A;Coss-references: UNIPROT:P21581; UNIPARC:UP1000144090; GB:M59966; NID:9206861; PIDN:
B;Lu, H.S.; Clogston, C.L.; Wyypych, J.; Fausset, P.R.; Lauren, S.; Mendiaz, E.A.; Zeebo,
A;Pitle: Amino acid sequence and post-translational modification of stem cell factor ison
A;Reference number: A39805; MUID:91217037; PMID:1708771
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C;Species: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: S70367,
R;Pecitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
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57.1%; Score 721; DB 2; Length 20
Best Local Similarity 79.8%; Pred. No. 1.1e-50;
Matches 138; Conservative 15; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stem cell factor short form precursor - quail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 'E'.27-190 cLUA>
A;Cross-references: UNIPARC:UP1000014F57C
C;Superfamily: mouse mast cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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Stem cell factor precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S58313
R;McInnes, C.J.; Logan, M.; Falconer, V.M.; Rawlins, P.; Huntly, J.; Haig, D. submitted to the RMBL Data Library, August 1995
A;Description: Molecular cloning and biological activity of ovine stem cell factor. A;Reference number: S58313
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA

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C; Superfamily: mouse mast cell growth factor
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JN0637
stem coll factor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0637
R;Zhou, J.H.; Ohtaki, M.; Sakurai, M.
Gene 127, 269-270, 1993
A;Title: Sequence of a cDNA encoding chicken stem cell factor.
A;Recension: JN0637; MJD:93273244; PMID:7684722
A;Accession: JN0637
A;Molecule type: mRNA
A;Residues: 1-287 <ZHO>
A;Molecule type: mRNA
A;Residues: 1-287 <ZHO>
A;Accession: JN0637
A;Coss-references: UNIPROT:Q09108; UNIPARC:UPI000013563C; GB:D13516; NID:g391648; PIDN:
A;Experimental source: brain
C;Superfamily: mouse mast cell growth factor
C;Keywords: growth factor; transmembrane protein
C;Keywords: growth factor; transmembrane predicted <SIG>
F;26-287/Product: stem cell factor #status predicted <MMT>
F;226-248/Domain: transmembrane #status predicted <TWM>
A; Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell fa A; Reference number: S70366; MUID:96283808; PMID:8679698
A; Accession: S70367
A; Molecule type: mRNA
A; Residues: 1-253 <PET>
A; Residues: 1-253 <PET>
A; Residues: 1-253 <PET>
A; Cross-references: UNIPARC:UPI000002B34F; EMBL:U43079; NID:g1150877; PIDN:AACS9934.1; C; Superfamily: mouse mast cell growth factor
C; Keywords: growth factor; transmembrane protein
C; Keywords: growth factor; transmembrane protein
F; 1-25, Domain: signal sequence #status predicted <SIG>
F; 26-253 Product: stem cell factor short form #status predicted <MAT>
F; 192-216/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKROP-SLTRAVENIQIN--EEDNEI 232
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                                                                                                                                                                                                                                                      Query Match 47.9%; Score 605; DB 2; Best Local Similarity 49.8%; Pred. No. 2.9e-41; Matches 126; Conservative 48; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.3%; Score 584; DB 2; 44.6%; Pred. No. 1.7e-39;
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Cybate: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
CyAccession: 870366
RyPetitte, J.N.; Kulik, M.J.
Biochim. Biophys. Acta 1307, 149-151, 1996
A;Title: Cloning and characterization of cDNAs encoding two forms of avian stem cell far
A;Reference number: 870366; MUID:96283808; PMID:8679698
A;Recension: 870366
A;Rolecule type: mRNA
A;Residues: 1-287 <PRT>
A;Cross-references: UNIPARC:UPI000013563D; EMBL:U43078; NID:g1150875; PIDN:AAC59933.1; 1
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C;Species: 22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accesion: S22052
R;Lu, H.S.; Clogston, C.L.; Wypych, J.; Parker, V.P.; Lee, T.D.; Swiderek, K.; Baltera J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 1-13;14-30;31-46;47-59;60-86;87-95;96-107;108-124 <LUH>
A;Cross-references: UNIPROT:Q7M4N8; UNIPARC:UP10000179563; UNIPARC:UP10000179564; UNIPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Post-translational processing of membrane-associated recombinant human stem cel
A;Reference number: S29052; MUID:92398336; PMID:1381905
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121 DKNKDPIKENGHLYEEDRFIPENFFRLFNRTIEVYKEFADSLDKNDCIMPSTVBTPENDS 180
181 RVAVTKTISPPPVAASSLRNDSIGSNTSSNSNKRALGPISSSSLQGISIALTSLLSLLIG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 MDSLPNHCWLHLMVPBFSRSLHNLLQKFVDISDMSDVLSNYSIINNLTRIINDLMACLAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDVLPSHCWISEMVVQLSDSLTDLLDKF---SNISEGLSNYSIIDKLVNIVDDLVECVKE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 NSSKD-LKKSFKSPEPRLFTPEEFFRIFNRSIDAPKDFVVASBTSDCVVSSTL-SPEKGK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Coturnix coturnix (quail)
C,Date: 06-Dec-1996 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKAQTWIITCPCLQLLLINPLVKTQSSCGNPVTDDVNDIAKLVGNLPNDYLITLKYVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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C.Keywords: growth factor; transmembrane protein
P;1-25/Domain: signal sequence #status predicted <SIG>
P;26-287/Product: stem cell factor long form #status predicted <MAT>
P;26-250/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                         287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 FILGVIYWKKTHPKSRPESNETTQCHGCQBENEISMLQQKEKEHLQV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.2%; Score 583; DB 2; Length 287; Best Local Similarity 44.3%; Pred. No. 2e-39; Matches 127; Conservative 47; Mismatches 71; Indels
                                                                                                                                           241 FILGALYWKKTHPKSRPESNETIQCHGCQEENEISMLQQKEKEHLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Mismatches
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Arch. Biochem. Biophys. 298, 150-158, 1992
A;Title: Post-translational processing of m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stem cell factor - human (fragments)
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Matches 127; Conservative
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Job

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time : 21.2479 secs
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A35971
master of the control of the contr
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B35971
mag to the factor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: B35971
C;Accession: B35971
R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R;Williams, D.E.; Eisenman, J.; Baird, A.; Rauch, C.; Van Ness, K.; March, C.J.; Park, I.R;Hite: Identification of a ligand for the c-kit proto-oncogene.
A;Reference number: A35971
A;Reference number: A35971
A;Accession: B35971
A;Residues: 1-51.<WIL)
A;Residues: 1-51.<WIL)
A;Residues: 1-51.<WIL)
C;Superfamily: mouse mast cell growth factor
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                    1 BGICRNRVTNNVK-------30
                                                                                                                                                                                                                               26 EGICRNRYTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 DKFSNISEGLSNYSII-----DDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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13.7%; Score 172.5; DB 2; Length 49;
Best Local Similarity 73.5%; Pred. No. 2e-07;
Matches 36; Conservative 4; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                 Query Match 38.9%; Score 491.5; DB 2; Length 124; Best Local Similarity 72.3%; Pred. No. 1.5e-32; Matches 107; Conservative 0; Mismatches 0; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
13.9%; Score 175.5; DB 2; Length 51;
Best Local Similarity 72.3%; Pred. No. 1.2e-07;
Matches 34; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ICGNPVTDNVXDITKLVANLPNDYMITLNYVAGMDVLPS-WWLDDMI 48
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Search completed: February 22, 2006, 18:20:28

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181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER 240
181 GDSSLHWAAMALPAFFSLIIGFAFGALYWKKRQPSLTRAVENIQINEDDNEISMLQEKER 240
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rattus norv
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felis silve
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1262
1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQEKEREFQEV 245
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 GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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08MWP2_PLAFA 08MWP1_PLAFA 08MWP1_PLAFA 09MML4_ARATH 02403_PLABE 067417_PLARE 07417_PLARE 07417_PLARE 05CR06_CRYPV 05CR06_C	T 988 TED BEG T	SCOTE 1255; Pred. No. 1.1 1; Mismatches NPLVKTEGICRNRV	FFRIFNRSID
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MEDLINE-22388257; PubMed=12477927; DOI 1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Allausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Districtenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., McWam P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,
Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORM 2).
MEDLINE=99160429; PubMed=10049787; DOI=10.1006/bbrc.1999.0260;
Blair H.C., Julian B.A., Cao X., Jordan S.B., Dong S.S.,
"Parathyroid hormone-regulated production of stem cell factor in human osteoblasts and osteoblast-like cells.";
Bjochem. Biophys. Res. Commun. 255:778-784(1999).
                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLECTIDE SEQUENCE (ISOFORM 1).
MEDLINE=91004219; PubMed=2208279; DOI=10.1016/0092-8674(90)90301-T;
Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz B.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher E.F., Erjavec H.O., Herrera C.J., Wpych J., Sachdev R.K.,
Pope J.A., Leslie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
"Primary structure and functional expression of rat and human stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92360843; PubMed=1379846;
Toyota M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;
Tayota M., Hinoda Y., Itoh F., Tsujisaki M., Imai K., Yachi A.;
"Expression of two types of kit ligand mRNAs in human tumor cells.";
Int. J. Hematol. 55:301-304(1992).
-i- FUNCTION: Stimulates the proliferation of mast cells. Able to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE (ISOFORM 2).
PubMed=1724381;
Anderson D.M., Williams D.E., Tushinski R., Gimpel S., Eisenman J., Cannizzaro L.A., Aronson M., Croce C.M., Huebner K., Cosman D.;
Alternate splicing of mRNAs encoding human mast cell growth factor and localization of the gene to chromosome 12q22-q24.";
Cell Growth Differ. 2:373-378(1991).
                 Surface Control of the Control of the Control of the Control of Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1)
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   273 AA
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell factor DNAB.";
Cell 63:203-211(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
HUMAN
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ISOId=P21583-2; Sequence=VSP 006022;
-!- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-!- PTM: A soluble form is produced by proteolytic processing of isoform in the extracellular domain.
-!- SIMILARITY: Belongs to the SCF family.
-!- DATABBASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MGFID142.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Cycoplasmic (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
By similarity.
FyrdevSyrkFFMLPPVAASSLRNDSSSSNR -> G (in isoform 2).
Fride-VSP_006022.
augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins.
SUBUNIT: Homodimer, non-covalently linked (Probable).
SUBCELLULAR LOCATION: Type I membrane protein (1soforms 1 and 2). Also exists as a secreted soluble form (1soform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure; Alternative splicing; Cell adhesion; Glycoprotein;
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128 K -> R (in Ref. 3 and 4; AAK92486).
134 L -> P (in Ref. 3 and 4; AAK92486).
30899 MW; 19FD362CB59C6607 CRC64;
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MINIO 1894/95; ...

GO; GO:0005886; C:plasma membrane; NAS.

GO; GO:0008283; P:setem cell factor receptor binding; NAS.

GO; GO:0008283; P:cell proliferation; TAS.

GO; GO:0007165; P:seignal transduction; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR012351; Cytokine 4 hix.

InterPro; IPR003452; SCF:

PANTHER; PTRR1574; SCF: 1.

PEam; PP02404; SCF: 1.
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Extracellular (Potential).
Potential.
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Name=1; Synonyms=SCF248;
IsoId=P21583-1; Sequence=Displayed;
Name=2; Synonyms=SCF220;
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EMBL; AF119835; AAA22048.1; -; mRNA.
EMBL; AF400436; AAK22485.1; -; mRNA.
EMBL; AF400437; AAK22486.1; -; mRNA.
EMBL; BC069733; AA469783.1; -; mRNA.
EMBL; BC069783; AA469783.1; -; mRNA.
EMBL; BC069797; AA469793.1; -; mRNA.
EMBL; BC074725; AA47725.1; -; mRNA.
EMBL; S42571; AA47255.1; -; mRNA.
FIR; B61190; B61190.
PIR; B61190; B61190.
PIR; B61190; B61190.
ENBR; ASSY4; A/B/C/D=26-166.
PDB; IEXEX; X-ray; A/B/C/D=26-166.
PDB; IEXEX; X-ray; A/B/C/D=26-166.
PDB; IEXEX F. X-ray; A/B/C/D=26-166.
PDB; IEXER; X-ray; A/B/C/D=26-166.
PDB; IEXER; X-ray; A/B/C/D=26-166.
PDB; IEXER; X-ray; A/B/C/D=26-166.
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ALTERNATIVE PRODUCTS:
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MIM; 184745; -.
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A Murray J.D., Bowling A.T.;
Murray J.D., Bowling A.T.;
I "A primary Human-Horse comparative gene map.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
I Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
I FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
I SUBGELLUIAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
I SUBCATE SOLUBLE form (By similarity).
I PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
I SIMILARITY: Belongs to the SCF family.
                                                                                                                  MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISECLSNYSIIDKLVNIVDDLVECVKENSS
                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKOYMITLKXVPG
                                                                                                                                                                         KOLKKS FKS PEPRLFTPEBFFRI FURSIDAFKD FVVAS BTSDCVVSSTLSPEKG-----
                                                                                                                                                                                       KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                        OSFMD2; O62765; Q95WG3; Q95MG8; Q9NIX5; 28-PEB-2003 (Rel. 41, Created) 28-PEB-2003 (Rel. 41, Latt sequence update) 28-PEB-2003 (Rel. 47, Latt sequence update) 10-MAY-2005 (Rel. 47, Latt annotation update) Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Wast cell growth factor) (MGF).

Name=KITLG; Synonyms=MGF, SCF;
Equus caballus (Horse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Laurasiatheria; Perissodactyla; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.; "An equine sequence homologous to stem cell factor (KIT-ligand)."; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 4-264.
Terry R.R., Mickelson J.R., Schmutz S., Cothran E.G., Bailey "Equus caballus mast cell growth factor (MGF)."; Submitted (JUL-201) to the EMBL/enBank/DDBJ databases.
            Length 273;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE OF 107-202 AND 227-274.
Terry R.R., Bailey B.F., Cothran B.G., "Fuduation of MGF as the candidate gene for Appaloosa Fubulited (APR-2001) to the EMBL/GenBank/DDBJ databases.
         97.5%; Score 1231; DB 1;
89.4%; Pred. No. 9.4e-89;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                               274 AA
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        Query Match
Best Local Similarity 89.4
Matches 244; Conservative
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n; Growth factor; Signal; Transmembrane.
Potential.
Kit ligand.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
N-linked (GlcMac. .) (Potential).
By similarity.
Q -> P (in Ref. 2).
Missing (in Ref. 2).
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P79169;
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2003 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-MAM-2005 (Rel. 1)
110-MAM-2005 (MAST 1)
110-MAM-2005 (MAST 2)
110-MAST 2)

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96C1D4C9059132F2 CRC64;
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EMBL; AF651498; AAC97076.1; -; mRNA.
EMBL; AF367704; AAK63249.1; -; Genomic_DNA.
EMBL; AF367706; AAK63250.1; -; Genomic_DNA.
EMBL; AF30770; AAF35716.1; -; Genomic_DNA.
EMBL; AF30770; AAF36716.1; -; Genomic_DNA.
EMBL; AF130770; AAF36716.1; -; Genomic_DNA.
EMBL; AF130770; AAF36716.1; -; Genomic_DNA.
INTERPO; IPR012351; Cytokine_4_hlx.
INTERPO; IPR012351; Cytokine_4_hlx.
INTERPO; IPR03452; SCF.
INTERPOSATION SCF.
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----KAKAVPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK 211
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                                      TISSUB-Uterus;

MEDLINE-94146218; PubMed=7508758;

MEDLINE-94146218; PubMed=7508758;

Zhang Z., Anthony R.V.;

In coalization within the uterus.";

Biol. Reprod. 50:95-102(1994).

I. FORNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines.

I. SUBUNIT: Homodimer, non-covalently linked (Probable).

I. SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).

I. TYM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).

I. SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NAY-2005 (Rel. 35, Last annotation update)
11-NAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGP).
Name=KITLG; Synonyms=MGF;
Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butheleostomi;
Nammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
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Kit ligand.

Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.
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                                                                                                                     241 KQPNLTRTVENIQINEEDNEISMLQEKEREPQEV
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InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth f STGNAL
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PIR; 146575; 146575.
SWR; Q29030; 29-161.
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                                                    NUCLECTIDE SEQUENCE (ISOFORMS 1 AND 2).
MEDLINE=97069946; PubMed=8912926;
Dunham S.P., Onions D.E.;
"The cloning and sequencing of cDNAs encoding two isoforms of feline stem cell factor.";
                                                                                                                                                      DNA Seq. 6.233-237(1996).

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).
-!- SUBGURIT: Homodimer, non-covalently linked (Probable).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2) Also exists as a secreted soluble form (isoform 1 only) (By similarity).
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

N-linked (GlcNAc. ..) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.
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SMR; P79169; 29-161.
InterEro; IPR012351; Cytokine_4_hlx.
InterPro; IPR003452; SCF.
PANTHER, PTRA11574; SCF; 1.
Pfam; PF02404; SCF; 1.
Alternative splicing; Cell adhesion; Glycoprotein; Growth factor; Signal; Transmenbrane.
SIGNAL.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P79169-2; Sequence=VSP 006021;
-!- PTM: A soluble form is produced by proteolytic processing of
  isoform 1 in the extracellular domain (By similarity).
-!- SIMILARITY: Belongs to the SCP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 83.3%; Score 1051.5; DB 1; Length 274; Local Similarity 76.6%; Pred. No. 1.3e-74; Nes 210; Conservative 17; Mismatches 18; Indels 29;
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C5B78DB4791237BE CRC64;
                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P79169-1; Sequence=Displayed;
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                                                                                                KDLKKSFKSPEPRLFTPBEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG---- 174
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                   MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota; Metazoa; Metazoa; Chordata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE=22831116; PubWed=12951073; DOI=10.1016/j.bbrc.2003.08.025;
Hirokawa Y.S., Watenabe M., Shiraishi T.;
"The 3'UTR of stem cell factor suppresses protein expression from a cotransfected vector.";
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81.1%; Score 1023; DB 2; Length 245;
Best Local Similarity 80.4%; Pred. No. 2e-72;
Matches 197; Conservative 18; Mismatches 30; Indels
 Indels
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EMBL; AB105879; BAC84980.1; -; mRNA.
SEQUENCE 245 AA; 27681 MW; 9615130876AC9D52 CRC64;
                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Stem cell factor KL-2.
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Q54A14;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Shiba; TISSUE-Brain;

Yanaqisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

Yanaqisawa N., Tanaka S., Yamanouchi K., Tojo H., Tachi C.;

"Identification of splicing isoforms of caprine stem cell factor
"Identification of splicing isoforms of the two major isoforms,
gSCF825 and gSCF741, in the brain and the skin of adult and fetal
"I Shiba goats, Gapra hirtus.";
Submitted (MAR-1997) to the WBL/GenBank/DBBJ databases.

-I- FUNCTION: Stimulates the proliferation of mast cells. Able to
augment the proliferation of both myealoid and lymphold
hematopoietic progenitors in bone marrow culture. Mediates also
cell-cell adhesion. Acts synergistically with other cytokines,
probably interleukins (By similarity).

-I- SUBGRILUMAR LOCATION: Type I membrane protein. Also exists as a
secreted soluble form (By similarity).

-I- SUBCLIULAR LOCATION: Type I membrane protein. Also exists as a
secreted soluble form (By similarity).

-I- FTM: A soluble form is produced by proteolytic processing of the
extracellular domain (By similarity).

-I- SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                            factor) (SCF) (Mast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor; Signal; Transmembrane
                                                                                                                                                                                                                                                  Capra hircus (Goat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi.
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GlcNAc. . .) (Potential) (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kit ligand.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Cytoplasmic (Rotential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1021.5; DB 1; Length
; Pred. No. 3e-72;
20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BBFE669A509EF65D CRC64;
                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit Ligand precursor (C-kit ligand) (Stem cell growth factor) (MGF).
Name=KITLG; Synonyms=SCF;
                                                    274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB002152; BAB71753.1; -; mRNA. SMR; Q95M19; 29-161.
InterPro; IPR012351; Cytokine_4_hlx. InterPro; IPR003452; SCF.
PANTHER; PTHR11574; SCF; 1.
PÉan; PP02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth fac
                                                    PRT;
                                                                                                                                                                                                                                                                                                                         Pecora; Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 N-
196 N-
114 BY
164 BY
31053 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.98;
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Matches 204; Conservative
                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 AA;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       removed.
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RESULT 7
SCF_CAPHI
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181 TKPFMLPPVAASSLRNDSSSSNRKASNSIEDSSLQWAAVALPAFFSLVIGFAFGALYWKK 240
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Isocia-Q28132-2; Sequence-VSP 006020;
PTM: A soluble form is produced by proteolytic processing of isoform in the extracellular domain (By similarity).
POLYMORPHISM: The roan locus is responsible for the coat coloration of Belgian Blue and Shorthorn cattle. The solid-colored and white animals are homosygotes, and the roan animals, with intermingled colored and white hairs, are heterozygous. The roan phenotype is due to the Asp-218 mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                        -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>۾</u>
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Spleen;
MEDLINE=94339176; PubMed=7520283; DOI=10.1016/0167-4889(94)90084-1;
Zhou J., Hikono H., Ohtaki M., Kubota T., Sakurai M.;
"Cloning and characterization of cDNAs encoding two normal isoforms bovine stem cell factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mediates also
                                                                                                                                                                                            SCF_BOVIN STANDARD; PRT; 274 AA.
028132; Q9TU74;
028122; Q9TU74;
028-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor) (MGF).
Name-KITLG; Synonyms-SCF;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kudo T.;
Rudo T.;
"Bovine counterpart of stem cell factor.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 204-239, AND VARIANT ASP-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                              RQPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                             241 KQPNLTRTVENRQINEEDNEISMLQEKEREFQEV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q28132-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1223:148-150(1994)
                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                   Pecora; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KOLKKSFKSPRPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                   Kit ligand.

Extracellular (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).

N-linked (GlcNAc. . .) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 MDVLPSHCWISEMVEQLSVSLTDLLDKFSNISEGLSNYCIIDKLVKIVDDLVECMEEHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------IGPAFGALYWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0106220; Q8SPM6;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 29, Last annotation update)
10-MAY-2005 (Rel. 29, Last annotation update)
11 Agrand precursor (C-kit ligand) (Stem cell factor) (SCF) (Mast
cell growth factor) (MGF).
Name=KXTLG; Synonyms=MGF;
Canis familiaris (DOG).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                     EMBL; D28934; BAA06061.1; -; mRNA.

EMBL; AB033716; BAA94808.1; -; mRNA.

FMRL; AB120154; AAD55355.1; -; Genomic_DNA.

FMRL; A27571; S47571.

SMR; Q28132; 29-161.

InterPor; IPR012351; Cytokine_4_hlx.

InterPor; IPR03452; SCP; 1.

PANTHER; PTHR1574; SCP; 1.

PEam; PF0404; SCF; 1.

PALE-INDERING SPlicing; Cell adhesion; Glycoprotein; Growth factor; Polymorphism; Iransmembrane.

SIGNAL

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.7%; Score 1018.5; DB 1; Length 274; Best Local Similarity 74.1%; Pred. No. 5.2e-72; Matches 203; Conservative 20; Mismatches 22; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP 006020.
A -> D (in roan allele).
D6CIDDB77B0CB12B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROPSLTRAVENIQINEEDNEISMLQEKEREPQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 AA
SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                          isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                   218 218 i 274 AA; 31015 MW;
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                                                                                                                                                                                                                                                                      274
215
238
274
274
1145
1196
1114
203
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216
239
239
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145
196
299
68
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TOPO DOM
TRANSMEM
TOPO DOM
CARBOHYD
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SEQUENCE
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DISULFID
VARSPLIC
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                                                                                 removed.
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SCF_CANFA
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                                                181 TKPFWLDPVAASSLRNDSSSSNRKASNSIGDSNLQWAAMALPAFFSLVIGFAFGALYWKK 240
   121 ENVKKAPKSPELRLFTPEEFFRIFNRSIDAFKOLBTVASKSSECVVSSTLSPDKOSRVSV 180
                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Mustelidae,
Mustelinae, Mustela.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9SNI8; Q9SNN5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-Kit ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF).
Name=KITLG; Synonyms=SCF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY013712; AAG37434.1; -; mRNA.
EMBL; AF323757; AAK73366.1; -; mRNA.
SMR; Q95018; 29-161.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTRR1274; SCF; 1.
Pfam; PFR0444; SCF; 1.
Alternative splicing; Cell adhesion; Glycoprotein; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=Q9SN18-2; Sequence=VSP 006024;
--- PTW: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain (By similarity).
--- SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
(Potential).
(Potential).
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Extracellular (Potential).

Botential.

Cytoplasmic (Potential).

N-linked (GlCNAc. . .) (Poten
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                                                                                             245
                                                                                                                        274
                                                                                             ROPSLTRAVENIQINEEDNEISMLOEKEREFOEV
                                                                                                             241 KOPNLTRTVENIQINBEDNBISMLOEKEREFOEV
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                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                               Mustela vison (American mink).
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9667;
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239
239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
                                                                                                                                                                                                      MUSVI
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TRANSMEM
TOPO DOM
CARBOHYD
                                                                                           212
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CARBOHYD
CARBOHYD
DISULFID
                                 175
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                                                                                                                                                                      RESULT 10
SCF_MUSVI
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                                                                                                                                                                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDLKKSPKSPEPRLFTPBEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG---- 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                         -!- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
-!- PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity).
-!- SIMILARITY: Belongs to the SCP family.
                                                                                                                                                                                                              Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

N-linked (GlCNAc. .) (Potential).

By similarity.

By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor; Signal; Transmembrane
                                                                                  Shull R.M., Suggs S.V., Langley K.E., Okino K.H., Jacobsen F.W., Martin F.H.; action action (c-kit ligand) supports the survival of hematopoietic progenitors in long-term canine marrow culture."; Exp. Hematol. 20:1118-1124(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kit ligand.
Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, S53329; AAB24619.1; -; mRNA.
EMBL, AY094361; AAM16280.1; -; mRNA.
PIR; 146929; 146929.
SWR, O66220; 29-161.
Ensembl; ENSCAFC00000006091; Canis familiaris.
InterPro; IPR012351; Cytokine_4_hlx.
InterPro; IPR03452; SCF.
PANTHER; PTHR11574; SCF; 1.
Piam; PP02404; SCF; 1.
Cell adhesion; Glycoprotein; Growth factor; Signa SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1014.5; DB 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE=93106145; PubMed=1281786;
                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 17-274.
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74.8%;
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Best Local Similarity 74.8
Matches 205; Conservative
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215
238
274
                                             NUCLEOTIDE SEQUENCE.
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196
196
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29
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68
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274 AA;
Canis.
NCBI_TaxID=9615;
                                                             TISSUE=T-cel
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TRANSMEM
TOPO DOM
CARBÖHYD
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NCBI_TaxID=10116;
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                                                 164
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                                                                                                                                                                                                                                      181 TKPFMLPPVAASSLRNDSSSSNRKAANPLGDSNLQWAAMALPAFFSLVIGFAFGALYWKK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 VANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDK 103
                                                                                                                                                                                                                           KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDF-VVASETSDCVVSSTLSPEKG---- 174
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                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                  isoform 2).
//FIId=VSP_006024.
//FIId=VSP_016024.
S -> N (in Ref. 1; AAK73366).
S -> N (in Ref. 1; AAK73366).
EREPQEV -> RESFKRCNCGFYHTVLSYLGG (in Ref.
                                                                                                                                                     VANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDK
                                                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                   MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
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           (in
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Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, CR749222; CAH18078.1; -; mRNA.

SMR; Q68DZ2; 9-126.

G0; G0:0005173; F:stem cell factor receptor binding; IEA.

G0; G0:0005173; F:stem cell factor receptor binding; IEA.
           U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                  80.4%; Score 1014.5; DB 1; Length 274; 73.7%; Pred. No. 1.1e-71; rive 20; Mismatches 23; Indels 29;
           ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 1005; DB 2; Length 238; 87.4%; Pred. No. 5.1e-71; ive 0; Mismatches 1; Indels 2
By similarity.
DSRVSVTKPFMLPPVAASSLRNDSSSSNR
                                                                    1; AAK73366).
5AC1619014AE5E72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26667 MW; 7D6B1E487BE3709B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                         RQPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                     241 KQPNLTRTAENIQINEEDNEISMLQEKEREFQEV 274
                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last seq 25-OCT-2004 (TrEMBLrel. 28, Last annowypothetical protein DKFZp686F2250.
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                MW.
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Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Amygdala;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR003452; SCF.
Pfam; PF02404; SCF; Hypothetical protein.
                                                                                31035
                                                                                                                                                                                                                                                                                                                                                                             Q68D22 HUMAN PRELIMINARY;
                                                                                                             Local Similarity 73.7
hes 202; Conservative
                                        65
171
274
164
                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=DKFZp686F2250;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 AA;
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171
268
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DISULFID
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                                       CONFLICT
                                                                                SEQUENCE
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163
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LVNIVDDLVECVKENSSKOLKKSPRSPRPRLFTPREFFRIFNRSIDAFKDFVVASETSDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUCLEOTIDE SEQUENCE OF 1-201, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE-910-04219; PubMed=2208279; DOI=10.1016/0092-8674(90) 90301-T;
Martin F.H., Suggs S.V., Langley K.E., Lu H.S., Ting J., Okino K.H.,
Morris C.F., McNiece I.K., Jacobsen F.W., Mendiaz E.A., Birkett N.C.,
Smith K.A., Johnson M.J., Parker V.P., Flores J.C., Patel A.C.,
Fisher E.F., Exjavec H.O., Herrera C.J., Wypych J., Sachdev R.K.,
Pope J.A., Lealie I., Wen D., Lin C.-H., Cupples R.L., Zsebo K.M.;
Primary structure and functional expression of rat and human stem
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-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probabbly interleukins.
-!- SUBUNIT: Homodimer, non-covalently linked (Probable).
-!- SUBCINIT: Homodimer, non-covalently linked (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Buffalo; TISSUE=Liver;
MEDLINE=91217037; PubMed=170871;
Lu H.S., Clogston C.L., Wypych J., Fausset P.R., Lauren S.,
Mendiaz E.A., Zsebo K.M., Langley K.E.;
"Amino acid sequence and post-translational modification of stem factor isolated from buffalo rat liver cell-conditioned medium.";
J. Biol. Chem. 266:8102-8107(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification, purification, and biological characterization of hematopoietic stem cell factor from buffalo rat liver-conditioned
                                                                                                                                                                                                                                                                                                                                             245
                                                                                                                                                                                                                                                                                                                                             196 FSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKEREFQEV
                                                                                                                                                                                                                                                                                                                                                                                              FSLIIGFAFGALYWKKROPSLITRAVENIOINEEDNEISMLOEKEREFOEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Teramoto T., Nagashima M., Thorgeirsson S.S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P21581; Q9QWZ4; Q9Z2E7;
01-MAY-1991 (Rel. 18, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Kit ligand precursor (C-kit ligand) (Stem cell factor)
cell growth factor) (MGF) (Hematopoietic growth factor
Name=Kitlg; Synonyms-Mgf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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63:203-211(1990)
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STRAIN=C3H/B1; TISSUB=Brain; MEDLINE=9703359900247; MEDLINE=97032534; PubMed=8875893; DOI=10.1007/8003359900247; Graw J., Loester J., Neuhaeuser-Klaus A., Pretsch W., Schmitt-John T.; "Molecular analysis of two new Steel mutations in mice shows a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=102/E1 x C3H/E1;
MEDLINE=98025115; PubMed=9360640; DOI=10.1016/S1383-5726(97)00005-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANTS SER-122; PRO-193 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE (ISOFORM 1), AND VARIANTS PRO-193 AND SER-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transversion or an insertion.";
Mamm. Genome 7:843-846(1996).
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                                                                                                SCF MOUSE
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SCE MOUSE
ID SCE WOUSE
DT O1-WAD
DT 
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                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 KPFMLPPVAASSLRNDSSSSNRKAAKSPEDPGLQWTAMALPALISLVIGFAFGALYWKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                   Name=1; Synonyma=KL-1;
Isoda=P21581-1; Sequence=Displayed;
Name=2; Synonyma=KL-2;
Isoda=P21581-2; Sequence=VSP 006025;
--- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoiesis.
--- PTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
--- SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensemil; ENSKNOG0000005386; Rattus norvegicus.

EnterPro; IPR012351; Cytokine_4_hlx.

InterPro; IPR013452; SCF.

PANTHER; PTHR11574; SCF; 1.

Pfam; PF02404; SCF; 1.

Pfam; PF02404; SCF; 1.

Alternative splicing; Cell adhesion; Direct protein sequencing; Glycoprotein; Growth factor; Pyrrolidone carboxylic acid; Signal; Transmembrane.
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Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Pyrrolidone carboxylic acid.

N-linked (GlcNAc. .); partial.

N-linked (Probable).

O-linked (Probable).

O-linked (Probable).

N-linked (Probable).

N-linked (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoform 2).
/FTIGA-VSP 006025.
S -> P (in Ref. 1; AAD02828).
COP56527DC93FD27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
similarity).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.6%; Score 992; DB 1;
71.8%; Pred. No. 6.4e-70;
iive 18; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                           EMBL; AF071204; AAD02827.1; -; mRNA.
EMBL; AF071205; AAD02828.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                EMBL; MS9966; AAA42117.1; -; mRNA.
PIR; B35974; B35974.
SMR; P21581; 29-159.
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273 AA; 30712 MW;
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Matches 196; Conserv
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CARBOHYD
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NUCLECTIDE SEQUENCE (ISOFORM 1).
MEDLINE=93012940; PubMed=1383087;
MEDLINE=93012940; PubMed=1383087;
MILIAMS C.I., Bedell M.A., Resnick J.L., Eppig J.J., Handel M.A.,
Williams D.E., Lyman S.D., Donovan P.J., Jenkins N.A., Copeland N.G.,
"Developmental abnormalities in Steell7H mice result from a splicing defect in the steel factor cytoplasmic tail.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91004223; PubMed=1698558; DOI=10.1016/0092-8674(90)90304-W; Anderson D.M., Lyman S.D., Baird A., Wignall J.M., Eisenman J., Rauch C., March C.J., Boswell H.S., Gimpel S.D., Cosman D., Williams D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two cell associated forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of mast cell growth factor, a hematopoietin that active in both membrane bound and soluble forms."; Cell 63:235-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91160046; PubMed=1705866; DOI=10.1016/0092-8674(91)90326-T;
                                                                                                                                                                                                         P20876; P97332; 062224; 064222; 0921NS; 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Created) 01-MX-1991 (Rel. 18, Last sequence update) 10-MX-2005 (Rel. 47, Last annotation update) Kit ligand precursor (C. Ait ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Hematopoietic growth factor KL) (Steel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flanagan J.G., Chan D.C., Leder P.; Transmembrane form of the kit ligand growth factor is determined alternative splicing and is missing in the Sld mutant."; Cell 64:1025-1035(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bedell M.A., Copeland N.G., Jenkins N.A.;
whiltiple pathways for Steel regulation suggested by genomic and
sequence analysis of the murine Steel gene.";
Genetics 142:927-934(1996).
241 QSSLTRAVENIQINBEDNEISMLQQKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (2)
NUCLEOTIDE SEQUENCE (ISOPORMS 1 AND 2).
NWEDLINE-92330001; PubMed-1378327;
Huang E.J., Nocka K.H., Buck J., Besmer P.;
"Differential expression and processing of t
                                                                                                                                                                                      $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Kitlg; Synonyms=Kitl, Mgf, Sl, Slf;
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NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
STRAIN=WCB6F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the kit-ligand: KL-1 and KL-2.";
Mol. Biol. Cell 3:349-362(1992).
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MEDLINE-97002551; PubMed=8849898;
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NUCLEOTIDE SEQUENCE (ISOFORM 1).
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NUCLEOTIDE SEQUENCE (ISOFORM 1).
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                                                                                                            NUCLECTIDE SEQUENCE [LARGE SCALE MENA] (ISOFORM 1).

REAIN=C57BL/6J; TISSUB=Cerebellum;

REAIN=C57BL/6J; TISSUB=Cerebellum;

REAIN=C57BL/6J; TISSUB=Cerebellum;

REAIN=C57BL/6J; TISSUB=Cerebellum;

REA OKazaki Y., Furunc M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Onackenbush J.,

Baldarelli R., Dragani T.A., Matsuda H., Batalov S., Beisel K.W.,

RA Schriml L.M., Kawapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Ratak J.A., Rawaji H., Kawasawa Y., Kedierski R.M., King B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Ronagaya A., Kurochkin I.V., Reid J., Ring B.Z., Ringwald M.,

RA Magashima T., Numata K., Okido T., Pertea G., Pesole G.,

Reardo R., Magner L., Marchionni L., Marchionni L., Marchionni L.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayateu N.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer R., Sakaxume N., Sakaxume N., Sakaxume N.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

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RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An poking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
As paleron M., Soares M.B., Bonaldo M.F., Carannor T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wickernan K.J., Maake J.A., Gupt., Mullahy S.J.,
A Richards S., Worley K.C., Fale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.G., Schentz D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smilus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smilus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smilus D.E.,
Greenzellon and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                    5 of the murine Mgf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Graw J., Neuhauser-Klaus A., Pretsch W.;
"Detection of a point mutation (A to G) in exon 5 of the mu
gene defines a novel allele at the Steel locus with a weak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                 Mutat. Res. 382:75-78(1997).
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[11] NUCLEOTIDE SEQUENCE OF 1-201.

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKTOTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
MEDLINE=91004220; PubMed=1698556; DOI=10.1016/0092-8674(90)90302-U; Zsebo K.M., Williams D.A., Geissler E.N., Broudy V.C., Martin F.H., Atkins H.L., Hau R.-Y., Birkett N.C., Okino K.H., Murdock D.C., Jacobsen F.W., Langley K.E., Smith K.A., Takeishi T., Cattanach B.M., Galli S.J., Suggs S.V.; Rem cell factor is encoded at the Sl locus of the mouse and is the ligand for the C-kit tyrosine kinase receptor.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PURCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopolietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins. Synergistically with other cytokines, probably interleukins. Covalently linked (Probable). SUBCELDIAR LOCATION: Type I membrane protein (isoforms I and 2). Also exists as a secreted soluble form (isoform I only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL PROTEIN SEQUENCE OF 26-78.

MEDLINE=91004215; PubMed=1698553; DOI=10.1016/0092-8674(90)90297-R; Williams D.E., Elsenman J., Baird A., Rauch C., van Ness K., March C.J., Park L.S., Martin U., Mochizuki D.Y., Boswell H.S., Burgess G.S., Cosman D., Lyman S.D.; "Identification of a ligand for the c-kit proto-oncogene."; Cell 63:167-174(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stages of hematopoiesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOId=P20826-2; Sequence=VSP_006023;
-1- DEVELOPMENTAL STAGE: Acts in the early stages of hematopoies:
-1- FTM: A soluble form is produced by proteolytic processing of isoform 1 in the extracellular domain.
-1- SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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EMBL; $68999; CAA48778.1.; -; mRNA.
EMBL; $144724; -; NOT ANNOTATED CDS; Genomic_DNA.
EMBL; $144725; AAC52447.1; -; mRNA.
EMBL; $25381; CAA64667.1; -; mRNA.
EMBL; $29322; CAA64667.1; -; mRNA.
EMBL; $29322; CAA64667.1; -; mRNA.
EMBL; $10287; CAA71329.1; -; mRNA.
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IsoId=P20826-1; Sequence=Displayed;
Name=2; Synonyms=KL-2;
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EMBL; M57647; AAA39538.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE OF 26-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity .... Matches 197; Conservative
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ALTERNATIVE PRODUCTS:
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240
                                                                                                                                                                                                                                                                                            D SCF_SHEEP STANDARD; PRT; 267 AA.

C P79368; Q28591;

T 28-FEB-2003 (Rel. 41, Last sequence update)

T 28-FEB-2003 (Rel. 47, Last annotation update)

T 10-MAY-2005 (Rel. 47, Last annotation update)

T 10-MAY-2005 (Rel. 47, Last annotation update)

T 10-MAY-2005 (Rel. 47, Last annotation update)

T 28-FEB-2003 (Rel. 47, Last annotation update)

T 38-FEB-2003 (Rel. 47, Last annotation update)

T 38-FEB-2003 (Rel. 47, Last annotation update)

C ALA TIGAND AFFORMENT (C-Att ligand) (Stem cell factor) (SCF) (Mast cell growth factor) (MGF) (Fragment).

S 37-FEB-2003 (Rel. 47, Last annotation) (ScF) (Mast cell growth factor) (MGF) (Fragment).

S 37-FEB-2003 (Rel. 41, Last sequence update) (ScF) (Mast cell growth factor) (Mast ligand factor) (SCF) (Mast cell growth factor) (MGF) (Mast ligand factor) (SCF) (Mast cell growth factor) (SCF) (Mast cell growth factor) (MGF) (Mast ligand factor) (SCF) (Mast cell growth factor) (MGF) (Mast ligand factor) (SCF) (Mast l
                                                            -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                         181 KPFMLPPVAASSLRNDSSSSNRKAAKAPEDSGLQWTAMALPALISLVIGFAFGALYWKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: A soluble form is produced by proteolytic processing of the extracellular domain (By similarity). SIMILARITY: Belongs to the SCF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoletic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interleukins (By similarity).

SUBUNIT: Homodimer, non-covalently linked (Probable).

SUBCELLULAR LOCATION: Type I membrane protein. Also exists as a secreted soluble form (By similarity).
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MEDILINE-99263197; PubMed=1032863; DOI=10.1006/cyto.1998.0430;
MEDILINE-99263197; PubMed=10328863; DOI=10.1006/cyto.1998.0430;
MICTINGE C.J., Deane D., Thomson J., Broad A., Haig D.M.,
"The cloning and expression of the cDNA for ovine stem cell factor (kit-ligand) and characterization of its in vitro haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e
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MEDLINE=96413880; PubMed=8662240; DOI=10.1007/8003359900142;
Tiedall D.J., Quirke L.D., Galloway S.M.;
"Ovine stem cell factor gene is located within a syntenic group chromosome 3 conserved across mammalian species.";
Mamm. Genome 7:472-473(1996).
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Extracellular (Potential).
                                                                                                                                             QPSLTRAVENIQINEEDNEISMLQEKEREPQEV 245
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Stimulates the proliferation of mast cells. Able to augment the proliferation of both myeloid and lymphoid hematopoietic progenitors in bone marrow culture. Mediates also cell-cell adhesion. Acts synergistically with other cytokines, probably interlevins (By similarity).

-!- SUBUNIT: Homodimer, non-covalently linked (By similarity).

-!- SUBCELULIAR LOCATION: Type I membrane protein (isoforms 1 and 2) Also exists as a secreted soluble form (isoform 1 only) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCF (Fragment).
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                       (Potential). (Potential). (Potential). (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.5%; Score 990.5; DB 1; Length 267; Best Local Similarity 74.2%; Pred. No. 8.2e-70; Matches 198; Conservative 19; Mismatches 21; Indels 29.
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EWEL, AY247403; AAP03067.1; -; mRNA.

HSSP; P21583; 1SCF.

SNR, Q66419; 4-136.

GO; GO:0016020; C:membrane; IEA.

GO; GO:001513; F:setlam cell factor receptor binding; IEA.

GO; GO:0007155; F:setlam dehesion; IEA.

InterPro; IPR003452; SCF.

Pfam; PP02404; SCF; 1.

Roll adhesion; Transmembrane.

NON_TER
238 Potential.

267 Cytoplasmic (Potential).

90 N-linked (GlcMAc. .) (Pote 97 N-linked (GlcMAc. .) (Pote 145 N-linked (GlcMAc. .) (Pote 166 N-linked (GlcMAc. .) (Pote 167 N-linked (GlcMAc. .) (Pote 168 N-linked (GlcM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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FT NON_TER 164 AA; 18430 MW; GAFB3AS68730110D CRC64;
SQ SEQUENCE 164 AA; 18430 MW; GAFB3AS68730110D CRC64;
Query Match 59.7%; Score 754; DB 2; Length 164;
Best Local Similarity 99.3%; Pred; No. 2e-51;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy
 86 DKFSNISBGLSNYSIIDKLVNIVDDLVBCVKENSSI

 Db
 61 DKFSNISBGLSNYSIIDKLVNIVDDLVBCVKENSSI

 Qy
 146 RSIDAFKDFVVASETSDCVVSSTLSPEK 173

 Db
 121 RSIDAFKDFAVASETSDCVVSSTLSPEK 148

Search completed: February 22, 2006, 18:19:22 Job time : 127,212 secs

Sequence Seq

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Title: Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

Database

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                                                   US-09-604-325A-48
US-09-24-681-50
US-09-224-681-50
US-09-224-681-50
US-09-224-681-50
US-08-336-728A-50
US-08-336-728A-82
US-08-955-848A-82
US-08-955-848A-82
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US-08-9224-681-57
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-918-63
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9392, Ap
2, Appli
9, Appli
49, Appli
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1262
1 MKKTQTWILTCIYLQLLLFN......NBEDNBISMLQEKERBFQEV 245
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                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/FCOMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-224-681-63
US-09-335-221-63-63
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US-09-244-683-63
US-09-949-016-9392
US-09-949-016-9392
US-08-482-918-61
US-08-482-918-61
US-08-482-918-61
US-08-482-918-61
US-08-482-918-61
US-08-336-728A-49
US-08-336-728A-49
US-08-336-728A-61
US-08-336-728A-61
US-08-336-728A-61
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US-08-336-728A-61
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US-09-949-016-9394
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Maximum Match 100%
Listing first 45 summaries
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FELECOMMUNICATION INFORMATION:
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APPLICANT: Bosselman, Robert A.
APPLICANT: Suges, Sidney V.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suges, Sidney V.
APPLICANT: Suges, Sidney V.
APPLICANT: Bosselman, Rethod for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
TITLE OF INVENTION: Areans I. 0. Toole, Gerstein, Murray & Borun
STREET: Asson Sears Tower, 233 South Wacker Drive
COUNTRY: United States of America
STATE: Illinois
COUNTRY: United States of America
COMPUTER FADABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER FADABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SACTHMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICANTION DATE:
FILLIAND DATE:
                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                               61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                    KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                        GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER
                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
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FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
PILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
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Patent No. 6207454
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US-09-224-681-63
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                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
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1 Sequence 63, Application US/08336728A

1 Patent No. 6207802

2 GRERAL INPORMATION:

4 APPLICANT: Scabo, Krisztina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Buggs, Sidney V.

1 TITLE OF INVENTION: Stem Cell Factor

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 6606-6402

COUNTRY: United States of America

ZIP: 6606-6402

COUNTRY: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/336,728A

FILING DATE: 09-NOV-1994

PUTOR ADDRESSEPTION: 424
                                                                                                                                                                                                                                                                                              Length 245;
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Pred. No. 3.3e-125;
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100.0%; Score 1262; 1
Best Local Similarity 100.0%; Pred. No. 3.3
Matches 245; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
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                                                  TELEX:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                          MOLECULE TYPE: protein
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Sequence 63, Application US/09224683

Patent No. 6841147

GENERAL INFORMATION:

APPLICANT: Sugge, Sidney V.

APPLICANT: Buselman, Robert A.

APPLICANT: Sugge, Sidney V.

APPLICANT: Sugge, Sidney V.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1262; DB 2;
100.0%; Pred. No. 3.3e-125;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32957A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/449,182

APPLICATION NUMBER: 08/172,329

APPLICATION NUMBER: 08/172,329

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/882,255

FILING DATE: 25-NO'1992

APPLICATION NUMBER: 07/884,535

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/573,616

FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-09-635-251-63
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 245 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQEKER
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STATE: Illinois
COUNTRY: United States of America
ZIP: 6666-6402
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
FILING DATE: 07-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Suggs, Sidney V.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1262; DB 2;
100.0%; Pred. No. 3.3e-125;
tive 0; Mismatches 0;
                                                                                                                                                                                                01017/32956
  APPLICATION NUMBER: 07/537,198
FILING DATE: 11-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTONEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 63, Application US/09635251
Patent No. 6759215
GENERAL INFORMATION:
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6SEQUENCE CHARACTERISTICS: LENGTH: 245 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                  312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-336-728A-63
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US-09-635-251-63
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Gaps

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121 KOLKKSFKSPEPRLFTPREFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKGKAKNPP 180
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CORRESPONDENCE ADDRESSE:
COUNTY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/09/604,325A
FILING DATE: 1-Jun-2002
CURRENT APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-CT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/573,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32953
TELECOMMONICATION INFORMATION:
NUMBER: 11-JUN-1990
APPLICATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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100.0%; Score 1262; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.3e-125;
Matches 245; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                      APPLICANT: Zsebo, Krisztina M.
Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-09-604-325A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acide
TYPE: amino acide
                                                                                                                                                    US-09-604-325A-63
; Sequence 63, Application US/09604325A
; Patent No. 6852313
; GENERAL INFORMATION:
     241 BFQEV 245
                                               241 EFQEV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISBGLSNYSIIDKLVNIVDDLVBCVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1262; DB 2; Length 245; Best Local Similarity 100.0%; Pred. No. 3.3e-125; Matches 245; Conservative 0; Mismatches 0; Indels 0;
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01017/35136
                       CITY: Chicago
STATE: Illinois
COUNTXY: United States of America
ZIP: 6060-6402
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
FILING DATE: 25-NOY-1995
FILING DATE: 25-NOY-1992
FILING DATE: 10-OCT-1990
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/59,701
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/42,383
FILING DATE: 16-OCT-1989
ATPORNEY/AGENT INFORMATION:
NAME: Clough, DATA: 36,107
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
RELECHONE: 312/474-6300
TELECPANGE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS: LENGTH: 245 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-224-683-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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KDLKKSFKSPERLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 GDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLGEKER 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 MKKTQTWILITCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDSSLHWAAMALPALFSLIIGPAFGALYWKKRQPSLTRAVENIQINBEDNEISMLQEKER
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1262; DB 2; Length 262; 100.0%; Pred. No. 3.7e-125; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPSY MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/220,379B
FILLNG DATE: 28-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-220-379B-2

Sequence 2, Application US/08220379B

Patent No. 5525708

GENERAL INFORMATION:
APPLICANT: Lobell, Robert B

APPLICANT: Lobell, Robert B

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CytoMed/2
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NAME: Haley Jr, James F
REGISTRATION NUBBER: 27,794
REFERENCE/DCKET NUMBER: Cytch
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-596-9000
TELEPAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 BFQEV 245
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                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-09-949-016-9392
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FATER NO. 9812339

FATER NO. 9812331

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 9391

LENGTH: 262
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| Patent No. 681233
| GENERAL INFORMATION:
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REPERENCE: CLO01307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
                                                                                                     61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVBCVKENSS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKOVTKLVANLPKDYMITLKYVPG 77
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                                                                                                                                                                                                                                                                                                                               Sequence 9391, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 245; Conservative
                                                                                                                                                                   241 EFQEV 245
                                                                                                                                                                                                             241 EPQEV 245
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                US-09-949-016-9391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-949-016-9392
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1-248 SCF protein begins at amino acid 26; amino acid 1-25 include Met and leader sequences for membrane band form of hurecombinant SCF."
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                                                                                                                                                                                                                                                                     Indels 28; Gaps
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; Sequence 49, Application US/08482918
; Patent No. 6207417
; GENERAL INFORMATION:
    APPLICANT: Scebo, Krisztina M.
    APPLICANT: Suggs, Sidney V.
    APPLICANT: Martin, Francis H.
    TITLE OF INVENTION: Stem Cell Factor
    NUMBER OF SEQUENCES: 104
    CORRESSEN Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
    STATE: Illinois
    COUNTRY: United States of America
    COUNTRY: United Sta
                                                                                                                                                                                            Query Match 97.5%; Score 1231; DB 1; Length 273; Best Local Similarity 89.4%; Pred. No. 7.5e-122; Matches 244; Conservative 0; Mismatches 1; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-482-918-49
               ) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-628-428-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAWALPALFSLIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
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                                                                                                                                                                                                                                                                                                                                                  97.5%; Score 1231; DB 1; Length 273; 89.4%; Pred. No. 7.5e-122; tive 0; Mismatches 1; Indels 2
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; Sequence 9, Application US/08628428
; GENERAL INFORMATION:
; APPLICANT: Lu, Hsieng
   TITLE OF INVENTION: SCF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
; STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE: CA
COUNTRY: USA
ZIP: 9130-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy 
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LOCATION: 1..273
OTHER INFORMATION: /note= "NOTE: Mature full length
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LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                ) NAME/KEY: cleavage site
; LOCATION: 164..165
US-08-220-379B-2
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 89,4 Matches 244; Conservative
                                                                                                                       MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                                                                                                                                                     181 KPFWLPPVAASSLRNDSSSSNRKAKONPPGDSSLHWAAWALPALFSLIIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zeebo, Krisztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Bosselman, Robert A.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEB: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                        1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKOVTKLVANLPKDYMITLKYVPG
MKKTQTW1LTC1YLQLLLFNPLVKTEG1CRNRVTNNVKDVTKLVANLPKDYM1TLKYVPG
                                                                                       MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVBCVKENSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
                                                                                                                                                                                                                                                                                                                                                                      OPSLIRAVENIQINBEDNEISMLOBKEREFOEV 245
                                                                                                                                                                                                                                                                                                                                                                                               241 QPSLTRAVENIQINBEDNEISMLQEKEREFGEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 Sout CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIPLCATION DATA:
APPLICATION NUMBER: 08/49,653
FILING DATE: 24-MAY-1995
CLASSIPLCATION:
PRIOR APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 25-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
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FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
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US-03-224-681-49
; Sequence 49, Application US/09224681
; Patent No. 6207454
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                          175 ------KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
                                                                                                                                  1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                          1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                    28; Gaps
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APPLICANT: Seabo, Krieztina M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Suggs, Sidney V.
APPLICANT: Busgs, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBERS OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: 104
COUNTRY: Gago
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITT: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6066-6402
COUNTRY: United States of America
ZIP: 6066-6402
COUNTRY: United States of America
STATE: HBM PC compatible
OURDRY: Floppy disk
COMPUTER: PRADABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 312/474-6300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
                   Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.5%; Score 1231; DB 2; Length 273; Best Local Similarity 89.4%; Pred. No. 7.5e-122; Matches 244; Conservative 0; Mismatches 1; Indels 2
                                                            1; Indels
              Query Match 97.5%; Score 1231; DB 2;
Best Local Similarity 89.4%; Pred. No. 7.5e-122;
Matches 244; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
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Patent No. 6207417
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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; MOLECULE TYPE: protein
US-08-482-918-61
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Sequence 61, Application US/09224681

Patent No. 6207454

GENERAL INFORMATION:
APPLICANT: Sugge, Sidney V.
APPLICANT: Bosselman, Robert A.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
ITILE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
ITILE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
ITILE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
ITILE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
ITILE OF INVENTION: Transfer with Stem Cell Factor (SCF) Polypeptide
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
Illinois
COUNTRY: United States of America
Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANTON NUMBER: US/09/224,681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-0448
TENGTH: 273 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
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US-09-224-681-49
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US-09-224-681-61
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US-08-336-728A-48
; Sequence 48, Application US/08336728A
; Patent No. 6207802
; Patent No. 6207802
; APPLICANT: Seebo, Krisztina M.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.5%; Score 1231; DB 2; Length 273; Best Local Similarity 89.4%; Pred. No. 7.5e-122; Matches 244; Conservative 0; Mismatches 1; Indels 2:
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                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA: 07/573,198
FILING DATE: 11-JUN 1990
PRIOR APPLICATION DATA: 07/422,383
ATTONEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKTION DATA: 36,107
REFERENCE/DOCKTION DATA: 36,107
REFERENCE/DOCKTION INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-09-224-681-61
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STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago CONDTRY: United States of America COUNTRY: United States of America COMPUTE: Illinois COMPUTE: Eloppy disk MEDIUM TYPE: RADDABLE FORM: WEDIUM TYPE: RADDABLE FORM: WEDIUM TYPE: BAPENCATION DATA: PC-DOS/MS-DOS SOFTWARE: BAPENCATION DATA: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/336,728A TLING DATE: 20-NOV-1994

PRIOR APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/539,701
PRIOR APPLICATION DATE: 01-OCT-1990
PRIOR APPLICATION DATE: 01-OCT-1990
PRIOR APPLICATION DATE: 01/537,198
FILING DATE: 11-UNG-1990
PRIOR APPLICATION DATA: 10/742,383
FILING DATE: 16-OCT-1990
PRIOR APPLICATION DATA: 10/742,383
FILING DATE: 16-OCT-1990
PRIOR APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1990
PRIOR PATERIANT INFORMATION: TELEPRONE: 312/474-6300
FILING DATE: 312/474-6300
FILING DAT
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MOLECULE TYPE: protein

US-08-336-728A-48
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Search completed: February 22, 2006, 18:21:59 Job time : 29.697 secs

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February 22, 2006, 18:20:42; Search time 97.865 Seconds (without alignments) 1046.014 Million cell updates/sec
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1 MKKTQTWILTCIYLQLILFN......NBEDNBISMLQEKERBFQEV 245
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Biocceleration Ltd.
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US-10-688-845-87
US-10-608-845-87
US-09-005-243-49
US-09-224-663-49
US-09-224-663-49
US-10-175-608-49
US-10-175-608-49
US-10-620-642-61
US-10-620-642-61
US-10-620-642-61
US-09-224-683-48
US-09-052-48-48
US-10-175-608-48
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US-09-224-683-52
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Maximum Match 100%
Listing first 45 summaries
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        Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl 30

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ALIGNMENTS

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RESULT 3
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Facent No. US2002003191A1

GENERAL INFORMATION:

APPLICANT: Seabo, Krisztina M.

APPLICANT: Boseslman, Robert A.

APPLICANT: Busselman, Robert A.

APPLICANT: Busselman, Robert A.

APPLICANT: Busting M.

CORRESONDENCES: 104

CORRESONDENCES: 104

CORRESONDENCES: 104

CONTRY: Chicago

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

CONTRY: United States of America

CONTRY: United States of America

STATE: Illinois

CONTRY: United States of America

CONTRY: United States of America

STATE: Poppy disk

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Percentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/224,683

FILING DATE: 12-JAN-1998

CLASSIFICATION NUMBER: 08/49,653

FILING DATE: 24-MAY-1995

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/49,653

FILING DATE: 24-MAY-1995

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 Length 245;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1262; DB 3; Best Local Similarity 100.0%; Pred. No. 5.6e-114; Matches 245; Conservative 0; Mismatches 0;
TELECOMMUNICATION INFORMATION:
TELEFRAX: 312/474-6300
TELEFRAX: 312/474-0448
TELEFRAX: 312/476-048
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
US-09-005-243-63
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US-09-224-683-63
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 11linois
COUNTRY: Unlied States of America
ZIP: 60606-6402
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; Sequence 63, Application US/10175608
; Publication No. US20040181044A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
Suggs, Sidney V.
; Suggs, Sidney V.
APPLICATION NOTICES.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/599,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 14-MG-1990
PRIOR APPLICATION NUMBER: 07/531,198
FILING DATE: 11-UUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORIEY/ARENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
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Matches 245; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BFOEV 245
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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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Sugge, Sidney V.

Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESSEE: Marshall, O'Toole, Geratein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STREET: 6300 Sears Tower, 233 South Wacker Drive CUNTRY: United States of America
ZIP: 6066-6402
COMPUTRY: BADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRS: FLOPPY disk
COMPUTRS: FLOPPY disk
COMPUTRS: FLOPPY SYSTEM: PC-DOS/MS.DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1262; DB 5; Length 245; 100.0%; Pred. No. 5.6e-114; ive 0; Mismatches 0; Indels 0;
Publication No. US20040247578A1
GENERAL INFORMATION:
APPLICANT: Lotze, Michael T
APPLICANT: Tahara' Hideaki
TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
FILE REFERENCE: UPT-004
CURRENT PELLING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/418,865
PRIOR APPLICATION NUMBER: 60/418,865
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
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PILING DATE: 16-Jul-2003
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 63, Application US/10620642; Publication No. US/20050080250A1 GENERAL INFORMATION: RAPLICANT: Zeebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-688-845-87
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US-10-620-642-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDLKKSPEKSPEPRLFTPEEFFRIFNRSIDAPKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                        MEDIUM TITES FALORY GUBA
MEDIUM TITES FALORY GUBA
SOSTWARE: PREFAIL Release #1.0, Version #1.30
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 09/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/982,255
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/53,616
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/53,100
APPLICATION NUMBER: 07/53,100
APPLICATION NUMBER: 07/53,010
APPLICATION NUMBER: 07/53,010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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100.0%; Pred. No. 5.6e-114;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 63
SEQUENCE CHARACTERISTICS
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Best Local Similarity
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RESULT 4 US-10-688-845-87 ; Sequence 87, Application US/10688845

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0; Gaps :0;

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61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKTQTWILICIYLQLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.5%; Score 1231; DB 3; Length 273; 89.4%; Pred. No. 6.7e-111; ive 0; Mismatches 1; Indels 21
STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM:
MEDIUM TYE: Eloppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC comp
      6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 OPSLTRAVENIOINEEDNEISMLOEKEREFOEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
TILING DATE: 24 MAY-1995
CLASSIFICATION NUMBER: 09/449,653
FILING DATE: 25 NOV-1995
FILING DATE: 25 NOV-1992
FILING DATE: 25 NOV-1992
FILING DATE: 01-0CT-1990
FILING DATE: 01-0CT-1990
FILING DATE: 01-0CT-1990
FILING DATE: 24-AUG-1990
FILING DATE: 10-0CT-1990
FILING DATE: 11-0UN-1990
FILING DATE: 11-0UN-1990
FILING DATE: 11-0UN-1990
FILING DATE: 15-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, DAVIG M.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 312/474-6300
FILING DATE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 amino acids
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Best Local Similarity 89.4
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-005-243-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49, Application US/09005243
Sequence 10. US20020018763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bosselman, Robert A.
APPLICANT: Sugge, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
                           FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/689,701
FILING DATE: 10-CCT-1991
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGBNT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
          APPLICATION NUMBER: 09/635,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 245 amino acids TYPE: amino acid
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 245; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-005-243-49
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181 KPFMLPPVAASSLRNDSSSSNRKAKNPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
                                                                                                                                                                       121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                                                                                          KOLKKSPKSPEPRLFTPBEPFRIFNRSIDAFKDFVVASBTSDCVVSSTLSPBKG---- 174
                                                                                                                                                                                                                                                                                 -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/09224683

Patent No. US20020031491A1

GENERAL INFORMATION:
APPLICANT: Sugge, Sidney V.
APPLICANT: Sugge, Sidney V.
TITLE OF INVENTION: Stem Cell Pactor: Composition Claims NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: 104
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Saars Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
CUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,683
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FLILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/49,653
FILING DATE: 24-MAY-1995
CLASSIFICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/539,701
FILING DATE: 01-CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/53,616
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
RICHARY APPLICATION DATA: 07/422,383
FILING DATE: 16-CCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 01017/35136
TELEBPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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                                                                                                                                          Sequence 6.1. Application US/09005243
; Sequence 6.1. Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
    APPLICANT: Zeabo, Kristina M.
    APPLICANT: Bosselman, Robert A.
    APPLICANT: Buggs, Sidney V.
    APPLICANT: Martin, Francis H.
    TITLE OF INVENTION: Stem Cell Factor
    NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.5%; Score 1231; DB 3; Length 273; Best Local Similarity 89.4%; Pred. No. 6.7e-111; Matches 244; Conservative 0; Mismatches 1; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago STATE: Discours marker billy of STATE: Illinois COUNTRY: United States of America ZIP: 66060-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NATA: APPLICATION NUMBER: US/09/005,243
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PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION NUMBER: 07/589,701
PILING DATE: 01-OCT-1990
PRIOR APPLICATION NUMBER: 07/53,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION NUMBER: 07/53,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION NUMBER: 07/422,383
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REPERENCE/POCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
US-09-005-243-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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US-09-224-683-61

Sequence 61, Application US/09224683

Fatent No. US20020031491A1

Fatent No. US20020031491A1

GENERAL INFORMATION:

APPLICANT: Busselman, Robert A.

APPLICANT: Suggs, Sidney V.

APPLICANT: Martin, Francis H.

ITILE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STREET: G111inois

COUNTRY: United States of America

ZIP: 6606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILL CALLOND DATA:

STATEM DATE.

APPLICATION DATA:

FILL CALLOND DATA:

FILL CALLOND

FILL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
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APPLICATION NUMBER: 08/449,653
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids TYPE: amino acid STRANDEDNESS: single STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-09-224-683-49
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.4
Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MDVLPSHCWISEMVVQLSDSLTDLLDXFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 28; Gaps
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Suggs, Sidney V.
Martin, Francis H.

TITLE OF INVENTIONS Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
SIRBET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1231; DB 3; Length 273;
Pred. No. 6.7e-111;
0; Mismatches 1; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 OPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: 111inois
COUNTRX: United States of America
ZIO: 60606-6402
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        01017/35136
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 36,107
TELEFRAY: 312/474-6300
TELEFRAX: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 49, Application US/10175608; Publication No. US/0040181044A1; GENERAL INFORMATION: APPLICANT: Zeebo, Krisztina M.
                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.5%;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.4'
Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-09-224-683-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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US-10-175-608-49
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ATTORNEY/AGENT INFORMATION
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Best Local Similarity 89.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 244; Conservative
                                                                                                                                                                                                             CITY: Chicago
    GENERAL INFORMATION:
APPLICANT: Zsek
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTXLVANLPKDYMITLKYVPG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1231; DB 4;
Pred. No. 6.7e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPSLTRAVENIQINEEDNBISMLQEKEREFQEV 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch
al Similarity 89.4%; Score 1231; D
al Similarity 89.4%; Pred. No. 6.7e
244; Conservative 0; Mismatches
                                                        CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/175,608
FILING DATE: 16-Oct-2002
CLASSIFICATION: «Unfrown»
                                                                                                                                                                               FILING DATE: 07-ANG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
FILING DATE: 21-DEC-1993
FILING DATE: 21-DEC-1993
FILING DATE: 25-NOV-1992
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-0CT-1991
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-ANG-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-0CT-1899
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/635,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 273 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 244; Conserva
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Sequence 61, Application US/10175608 Publication No. US20040181044A1

RESULT 11 US-10-175-608-61

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MDVLPSHCWISEMVVOLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKIQIWILICIYLQLLLENPLVKIBGICRNRVINNVKOVIKLVANLPKOYMILKYVPG
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                                                                                               Gerstein, Murray & Borun
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/175,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1231; DB 4;
Pred. No. 6.7e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01017/35199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                           STATE: Illinots
COUNTRY: United States of America
ZIP: 60606-6402
MATLIN, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/635,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-AUG-2000
APPLICATION NUMBER: 09/486,546
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 10-APR-1991
APPLICATION NUMBER: 09/589,701
FILING DATE: 10-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/537,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
                                                                                             ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 16-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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9

Gaps

28;

Length 273; Indels

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MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                      121 KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKG----- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKTQTWILICIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ZBEED, ATBELLIA W.

BOSSELMAN, ROBERT A.

Suggs, Sidney V.

CITT. Chicago.

STRET: 6300 Sears Tower, 233 South Wacker Drive
CITT: Chicago.

STRET: 6100 Sears Tower, 233 South Wacker Drive
CITT: Chicago.

STRET: 6100 Sears Tower, 233 South Wacker Drive
CITT: Chicago.

STRET: 6100 Sears Tower, 233 South Wacker Drive
CITT: Chicago.

STRET: 6100 Sears Tower, 233 South Wacker Drive
CUNTRY: United States of America.

ZIP: 6060-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATION STREEN: PC-006/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/620,642

FILING DATE: 16-Jul-2003

CLASSIFICATION NUMBER: US/10/175,608

FILING DATE: 10-Jul-2000

APPLICATION NUMBER: 09/635,249

FILING DATE: 21-BC-1993

APPLICATION NUMBER: 08/172,329

FILING DATE: 22-NOV-1995

APPLICATION NUMBER: 09/684,535

FILING DATE: 22-NOV-1993

APPLICATION NUMBER: 09/589,701

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 09/589,701

FILING DATE: 10-APR-1990

APPLICATION NUMBER: 09/589,701

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: 09/593,616

FILING DATE: 24-AUG-1990
                                                                                                      1 Similarity 89.4%; Pred. No. 6.7e-111; PB 5; Similarity 89.4%; Pred. No. 6.7e-111; 44; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 OPSLIRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 QPSLTRAVENIQINEEDNEISMLQEKEREPQEV 273
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-620-642-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application US/10620642
Publication No. US20050080250A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
                                                                                                        Query Match
Best Local Simil
Matches 244; C
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US-10-620-642-61
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                                                                                        181 KPFMLPPVAASSLRNDSSSSNRKAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 240
        121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVT 180
                                                           -----KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR 212
                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/10620642
; Publication No. US20050080250A1
; GENERAL INFORMATION:
; APPLICANT: ZEBO, Krisztina M.
Bosselman, Robert A.
; Suggs, Sidney V.
Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSER Marfall, O'Toole, Gerstein, Murray & Bor STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURTY: Chicago
STATE: 11linois
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: 11 SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/620,642
FILING DATE: 16-Jul-2003
CLASSIFCATION NUMBER: US/10/15,608
FILING DATE: 16-OCL-2002
APPLICATION NUMBER: US/10/15,608
FILING DATE: 16-OCL-2002
APPLICATION NUMBER: US/486,546
FILING DATE: 10-DCC-1993
APPLICATION NUMBER: 09/635,249
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 07/982,255
FILING DATE: 21-DCC-1993
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-OCT-1991
APPLICATION NUMBER: 07/64,535
FILING DATE: 10-AFR-1991
APPLICATION NUMBER: 07/637,198
FILING DATE: 10-ARR-1991
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 16-OCT-1989
ATTORNEY/AGART INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 310,107
REFERENCE/DOCKET NUMBER: 310,107
REGISTRATION NUMBER: 310,107
REFERENCE/DOCKET NUMBER: 310,107
RESTREATION NUMBER: 310,107
RESTREATION NUMBER: 310,107
RESTREATION NUMBER: 310,107
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                                                                                                                                                                                         LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 312/474-0448
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US-10-620-642-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG 60
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| Sequence 48, Application US/09005243
| Sequence 48, Application US/09005243
| Patent No. US2002001863A1
| Patent No. US2002001863A1
| APPLICANT: Zsebo, Krisztina M. APPLICANT: Bosselman, Robert A. APPLICANT: Buggs, Sidney V. APPLICANT: Martin, Francis H. ITLE OF INVENTION: Stem Cell Factor NUMBER OF SEQUENCES: 104
| CORRESPONDENCE ADDRESS: 104
| CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinos
| COUNTRY: United States of America COUNTRY: United States of America STATE: IBM PC COMPATER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATER: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
| APPLICATION: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.5%; Score 1231; DB 5; Length 273; Best Local Similarity 89.4%; Pred. No. 6.7e-111; Matches 244; Conservative 0; Mismatches 1; Indels 2:
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELERCAMPONE: 312/474-6300
TELERCAMPONE: 312/474-6448
TELERAX: 312/474-0448
TELERAX: 312/474-0448
TELERAX: 4UNANOMN:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 QPSLTRAVENIQINEEDNBISMLQBKGREFQEV 273
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                            US-10-620-642-61
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1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKKVPG 60
1 MKKTQTWILTCIYLQLLLENPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKKVPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 KPFMLPPVAASSLRNDSSSSNRKAKONPPGDSSLHWPAWALPALFSLIGFAFGALYWKKR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------KAKNPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.1%; Score 1226; DB 3; Length 273; Best Local Similarity 89.0%; Pred. No. 2e-110; Matches 243; Conservative 0; Mismatches 2; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-224-683-48

Sequence 48, Application US/09224683

Sequence 48, Application US/09224683

Sequence 48, Application US/0924683

Septent No. US20020013491A1

APPLICANT: Zsebo, Krisztina M.

APPLICANT: Bosselman, Robert A.

APPLICANT: Bosselman, Robert A.

APPLICANT: Martin, Francis H.

TITLE OF INVENTION: Stem Cell Factor: Composition Claims

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 QPSLTRAVENIQINEEDNEISMLQEKEREFGEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01017/34465
APPLICATION NUMBER: 09747, CLASSIFICATION NUMBER: 24-MAY-1995
CLLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/537,198
PILING DATE: 11-JUM-1990
PRIOR APPLICATION NUMBER: 07/422,383
PILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 310,107
REFERENCE/DOCKET NUMBER: 01017/34
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6300
TELEPHONE: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-09-005-243-48
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### STREET. # 6300 Sasts Tower, 233 South Wacker Drive

STREET. | ### State |
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Search completed: February 22, 2006, 18:26:56 Job time : 98.865 secs

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REFERENCE/DOCKET NUMBER: 01017/32958A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-MOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/589,701
FILING DATE: 10-CCT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 11-UN-1990
APPLICATION NUMBER: 07/537,198
FILING DATE: 11-COT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-10-353-783-63
Sequence 63, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
Bosselman, Robert A.
Bosselman, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Clough, David W. REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             February 22, 2006, 18:22:17 ; Search time 9.44904 Seconds (without alignments) 386.005 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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Sequence
Sequence
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1262
1 MKKTQTWILTCIYLQLLLFN......NEEDNBISMLQEKERBFQEV
5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US11_NBW_PUB.pep:*
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US-10-353-783-49

US-10-353-783-49

US-10-353-783-50

US-10-519-390-24

US-11-176-830-250

US-11-176-830-529

US-11-176-830-529

US-11-176-830-539

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US-11-176-830-539

US-11-176-830-531

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   version = 2006 E
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                               protein search, using
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published
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Maximum DB
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ALIGNMENTS

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Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: 4300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                  STREET: 6300 Sears Tower, 233 South Wacker Drive City: Chicago STATE: 111inois COUNTY: United States of America COUNTY: United States of America CONTY: 11000 SYSTEM: PC-DOS/MS-DOS SOOTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/353,783 FILING DATE: 28-Jan-2003 CLASSIFICATION: cUnknown>
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Result Š. 222210984654321 222210984654321

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121 KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKG----- 174
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US-10-353-783-61
is Sequence 61, Application US/10353783
is Sequence 61, Application US/10353783
is Sequence 61, Application No. US20050261175A1
is Publication No. US20050261175A1
is GENERAL INFORMATION:
is Martin, Francis H.
is TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
is CORRESPONDENCE ADDRESS:
is STREET: 6300 Sears Tower, 233 South Wacker Drive
CITTY: Chicago
is STREET: 6400 Sears Tower, 233 South Wacker Drive
COUNTRY: United States of America
is STATE: Illinois
is STATE: Illinois
is COUNTRY: United States of America
is GOMPUTER: EADABLE FORM:
is MEDIUM TYPE: FIORPY disk
is COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.5%; Score 1231; DB 6; Length 273; Best Local Similarity 89.4%; Pred. No. 1.3e-105; Matches 244; Conservative 0; Mismatches 1; Indels 2:
          APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
APPLICATION NUMBER: 07/53,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/53,198
FILING DATE: 11-0TM-1990
APPLICATION NUMBER: 07/42,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INPORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION INPORMER: 36,107
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAKE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-353-783-49
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KOLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVSSTLSPEKGKAKNPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: CIN.CAGO
STATE: 111inois
CONTRY: United States of America
COUNTRY: United States of America
CONTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFCATION NUMBER: 08/448,729
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
    TELEPHONE: 312/474-6300
TELEPRA: 312/474-6300
TELERA: 312/474-6348

TELERA: «Unknown»

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-353-783-63
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 273;
                                                                                                    STREET: 6300 Sears Tower, 233 South wacker Dilive CITY: Chicago STATE: 111inois COMPUTRY: United States of America COUNTRY: United States of America 21P: 6606-6402

COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk COMPUTER: IBM PD COMPAGABLE PORM:
MEDIUM TYPE: PLOS/MS-DOS SOFTWARE: Batentin Release #1.0, Version #1.30

CURRENT APPLICATION NDATA: 180/10/353,783

FILING DATE: 28-Jan-2003

CLASSIFICATION NUMBER: 08/448,729

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/684,535

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/692,555

FILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/533,616

FILING DATE: 10-OCT-1990

APPLICATION NUMBER: 07/533,198

FILING DATE: 11-OTT-1990

APPLICATION NUMBER: 07/533,198

FILING DATE: 11-OTT-1990

APPLICATION NUMBER: 07/422,383

FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 36,107

TELEPHONE: 312/474-6308

TELEPHONE: 312/474-6348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.1%; Score 1226; DB 6; Best Local Similarity 89.0%; Pred. No. 3.8e-105; Matches 243; Conservative 0; Mismatches 2;
                 TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-353-783-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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                     Version #1.30
                                                                   PRIOR DATE: 28-Jan-2003

PLING DATE: 28-Jan-2003

CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION WIDMER: 08/448,729

FILING DATE: 24-MAY-1995

APPLICATION NUMBER: 07/982,255

FILING DATE: 21-DEC-1993

APPLICATION NUMBER: 07/684,535

APPLICATION NUMBER: 07/684,535

FILING DATE: 10-APR-1991

APPLICATION NUMBER: 07/53,616

FILING DATE: 01-OCT-1990

APPLICATION NUMBER: 07/573,198

FILING DATE: 11-JUN-1990

APPLICATION NUMBER: 07/571,198

FILING DATE: 16-OCT-1989

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

RELECOMMUNICATION NUMBER: 36,107

RESISTRATION NUMBER: 36,107

RESISTRATION NUMBER: 36,107

RESISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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Best Local Similarity 89.4%; Pred. No. 1.3e-105;
Matches 244; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAECHLIR Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/353,783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-353-783-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/10353783
Publication No. US20050261175A1
GENERAL INFORMATION:
APPLICANT: Zsebo, Kristina M.
Bosselman, Robert A.
Suggs, Sidney V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 273 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-353-783-48
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Gaps

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ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6100 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 66606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/32958A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                               241 QPSLTRAVENIQINEEDNEISMLQEKEREFQEV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/353,783
FILING DATE: 28-Jan-2003
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 08/448,729
FILING DATE: 24-MAY-1995
APPLICATION NUMBER: 08/172,329
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 07/684,535
FILING DATE: 25-NOV-1992
APPLICATION NUMBER: 07/684,535
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/689,701
FILING DATE: 01-CT-1990
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-CT-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
                                                                                                                                                                                                                                                                                                 Bosselman, Robert A.
Suggs, Sidney V.
Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-353-783-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-JUN-1990
APPLICATION WINBER: 07/422,383
FILING DATE: 16-0CT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       APPLICANT: Zsebo, Krisztina M.
                                                                                                                                                                                        Sequence 50, Application US/10353783 Publication No. US20050261175A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 273 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/474-0448
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              GENERAL INFORMATION:
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1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG

Indels

APPLICANT: MEDEXGEN Inc.

APPLICANT: MEDEXGEN Inc.

APPLICANT: LEB, Hak-sup

APPLICANT: LEB, Hak-sup

APPLICANT: YI, Ki-Wan

APPLICANT: XIM, Jae-Youn

APPLICANT: XIM, Jae-Youn

APPLICANT: HEO, Youn-Hwa

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A proteins and the example muteins

TITLE OF INVENTION: Proteins and the example muteins

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

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TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of improving efficacy of biological response-modifying

TITLE OF INVENTION: A method of i ; OTHER INFORMATION: SCF: 63rd, 102nd, 110th, 115th, 116th, 119th, 126th, 129th, ; OTHER INFORMATION: 158th, 199th, 205th, 207th or 245th Phe is replaced by Val. US-10-519-390-24 121 KOLKKSPKSPEPRLFTPEEFFRIFNRSIDAFKOFVVASETSDCVVSSTLSPEKG----- 174 121 KOLKKSFKSPEPRLFTPEEFPRIFNRSIDAFKDFAVASETSDCVVSSTLSPEKDSRVSVT 180 145 61 DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSFREPRLFTPEBFFRIFN 120 -----KAK 177 178 NPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQE 237 85 9 61 MDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS 1 EGICRNRVINNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 1 MKKTQTWILTCIYLQLLLFNPLVKTEGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPG MDVLPSHCWISEMVVQLSDSLTD1LDXFSNISEGLSNYSIIDKLVNIVDDLVECVKENSS DKFSNISEGLSNYSIIDKLVNIVDDLVECVKRNSSKDLKKSPRPRLFTPEEFFRIFN 26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL Gaps Indels 28; Length 248; Query Match 87.1%; Score 1099; DB 6; 3 Best Local Similarity 88.3%; Pred. No. 1.5e-93; Matches 219; Conservative 0; Mismatches 1; 146 RSIDAFKDFVVASETSDCVVSSTLSPEKG------Sequence 24, Application US/10519390; Publication No. US20060008872A1; GENERAL INFORMATION: ORGANISM: Artificial Sequence FEATURE: 245 KEREFQEV 248 KEREFQEV US-10-519-390-24 61 98 238 241 TYPE: PRT 셤 셤 Š 임 ò a 셤 ò 셤 ò a ò g ò 셤 ò à ò

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Sequence 537, Application US/11176830

Fublication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Gantier, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION: MORBER: US/11/176, 830
CURRENT FILING DATE: 2005-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR FILING DATE: 2003-09-09
NUMBER: OF SEQ ID NOS: 1306
SOFTWARE: FRASESE FOR WINDOWS VETSION 4.0
SEQ ID NO 537
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DKPSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDIKKSFKSPEPRLFTPEEFFRIFN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 NPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPERPRLFTPEBFRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 RSIDAPKOPVVASETSDCVVSSTLSPEKG-------KAK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPPGDSSLHWAAMALPALPSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EGICKNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EGICRNRVINNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL 60
                                                                                                                                                                                                                                                                                                                                                                                                        26 EGICRNRVTNNVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLL
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                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                              Length 248;
                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                           Score 1097; DB 7; Pred. No. 2.2e-93; 1; Mismatches 1;
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 520
LENGTH: 248
                                                                                                                                                                                                                                                                                         Best Local Similarity 87.9%;
Matches 218; Conservative 1
                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-520
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                                    Sequence 206, Application US/11176830

Fublication No. US20060020116A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gantier, Lila

APPLICANT: Guyon, Thierry

APPLICANT: Drittanti, Lila

APPLICANT: Drittanti, Lila

APPLICANT: Usua Manuel

ITILE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding NU

TITLE OF INVENTION: Acid Molecules and Related Applications

CURRENT APPLICATION NUMBER: US/11/176,830

PRIOR APPLICATION NUMBER: 106/11/176,830

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 1306

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 206

LENGTH: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-176-830-520

Sequence 520, Application US/11176830

Sequence 520, Application US/11176830

Sequence 520, Application US/11176830

Sequence 520, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Gayon, Thierry
APPLICANT: Gayon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu FILE REPERENCE: 17109-012002 (922B)
CURRENT APPLICATION NUMBER: US/11/176,830

CURRENT FILING DATE: 2003-07-06

PRIOR APPLICATION NUMBER: 10/658,834

PRIOR FILING DATE: 2003-09-08

PRIOR APPLICATION NUMBER: 60/457,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RSIDAFKDFVVASETSDCVVSSTLSPEKDSRVSVTKPFMLPPVAASSLRNDSSSSNRKAK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSIDAPKDFVVASETSDCVVSSTLSPEKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA85450
DATABASE ENTRY DATE: 1996-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEREFQEV 245
                         -11-176-830-206
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; ORGANISM: Homo sapiens
US-11-176-830-529
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| Sequence 519, Application Wo. US2006020116A1
| GENERAL INFORMATION:
| APPLICANT: Gantier: Rene |
| APPLICANT: Outlant; Lila |
| APPLICANT: Drittant; Lila |
| APPLICANT: Drittanti, Lila |
| APPLICANT: Drittantion Release and Related Applications |
| TITLE OF INVENTION: Acid Molecules and Related Applications |
| TITLE OF INVENTION: Acid Molecules and Related Applications |
| TITLE OF INVENTION: Acid Molecules and Related Applications |
| TITLE OF INVENTION NUMBER: 10/658,834 |
| PRIOR PILING DATE: 2003-09-08 |
| PRIOR PILING DATE: 2003-09-09 |
| PRIOR PPLING DATE: 2003-09-09 |
| NUMBER OF SEQ ID NOS: 1306 |
| SEQ ID NO 519 |
| LENGTH: 248 |
| LENGTH
DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSFKSPEPRLFTPEEFFRIFN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDVKKSFKSPEPRLFTPEEFFRIFN 120
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                                                                                              RSIDAFKDFVVASETSDCVVSSTLSPEKG-
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05.11-17-6330-529
; Sequence 529, Application US/11176830
; Publication No. US20060020116A1
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APPLICANT: Gantier, Rene
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Usea, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
TITLE OF INVENTION: Acid Molecules and Related Applications
FILE REFERENCE: 17109-012002 (9228)
CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT PILING DATE: 2003-09-08
FRIOR FILING DATE: 2003-09-08
FRIOR FILING DATE: 2003-03-21
FRIOR FILING DATE: 2002-09-09
FRIOR APPLICATION NUMBER: 60/409,898
FRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 529
LENGTH: 248
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Sequence 536, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:
APPLICANT: Guntier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Drittanti, Lila
APPLICANT: Main Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu.
TITLE OF INVENTION: Acid Molecules and Related Applications
TITLE OF INVENTION NUMBER: US/11/176,830

CURRENT FILING DATE: 2005-07-06
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/457,135
FRIOR APPLICATION NUMBER: 60/459,898
FRIOR APPLICATION NUMBER: 60/409,898
FRIOR APPLICATION NUMBER: 60/409,898
FRIOR APPLICATION OF STEATED TO STEATE FARSTER FARSTER FILING DATE: 2002-09-09
SOFTWARE PRESTEE FOR Windows Version 4.0
SEQ ID NO 536
LENGTH: 248
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Best Local Similarity 87.9%; Pred. No. 2.7e-93;
Matches 218; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 RSIDAFKDFVVASETSDCVVSSTLSPEKG-----
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US-II-I/O BADDICATION US/11176830

Sequence 499, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Gard.

APPLICANT: Useda, Manuel

ITILE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Ni

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Ni

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Ni

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Ni

TITLE OF INVENTION: Acid Molecules and Related Applications

FILE REFERENCE: 1705-012002 (922B)

CURRENT FILING DATE: 2005-07-06

PRIOR PILING DATE: 2003-03-03

PRIOR PPLICATION NUMBER: 60/457,135

PRIOR PPLING DATE: 2003-03-03

PRIOR PRILING DATE: 2003-03-03

PRIOR PILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 1306

SOFTWARE FRAESEC
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Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Guyon, Thierry

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N

TITLE OF INVENTION: Acid Molecules and Related Applications
DKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKOLKKSFKSPEPRLFTPEEFFRIFN 145
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86.8%; Score 1095; DB 7;
Best Local Similarity 87.9%; Pred. No. 3.4e-93;
Matches 218; Conservative 1; Mismatches 1;
                                                                                                                 KEREFOEV 245
                                                                                                                                                      241 KEREFQEV 248
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ORGANISM: Homo sapiens
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US-11-176-830-500
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Sequence 538, Application US/11176830

Publication No. US20060020116A1

GENERAL INFORMATION:

APPLICANT: Gantier, Rene

APPLICANT: Griven, Thierry

APPLICANT: Griven, Thierry

APPLICANT: Griven, Thierry

APPLICANT: Griven, Thierry

APPLICANT: Wega, Manuel

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF INVENTION: Acid Molecules and Related Applications

TITLE OF ILING DATE: 2002-07-06

PRIOR APPLICATION NUMBER: 10/659,834

PRIOR APPLICATION NUMBER: 60/457,135

PRIOR PILING DATE: 2003-09-08

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 538

LENGTH: 248

MANUEL APPLICATION NUMBER: 60/409,898

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SEQ ID NO 538

LENGTH: 248

MANUEL APPLICATION NUMBER: PARTING NOS: 1306

SEQ ID NO 538

MANUEL APPLICATION NUMBER: PARTING NOS: 1306

SEQ ID NO 538

MANUEL APPLICATION NUMBER: PARTING 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 NPPGDSSLHWAAMALPALFSLIIGFAFGALYWKKRQPSLTRAVENIQINEEDNEISMLQE 237
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                                                                                                                                                                            1; Indels
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                                                                                                           Query Match

86.8%; Score 1096; DB 7;

Best Local Similarity 87.9%; Pred. No. 2.7e-93;

Matches 218; Conservative 1; Mismatches 1;
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Best Local Similarity 87.9%; Pred. No. 2.7e-93;
Matches 218; Conservative 1; Mismatches 1;
                        ; ORGANISM: Homo sapiens
US-11-176-830-536
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FILE REFERENCE: 17109-012002 (922B)

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CURRENT APPLICATION NUMBER: US/11/176,830
CURRENT FILING DATE: 2005-07-06
PRIOR PILING DATE: 2005-07-08
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/457,135
PRIOR PILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/409,898
PRIOR PILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 500
LENGTH: 248
                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-176-830-500
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KEREFQEV 248
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Search completed: February 22, 2006, 18:27:29 Job time : 10.449 secs